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March 31, 2005, 02:17:12 ; Search time 88.7903 Seconds (without alignments) 65.338 Million cell updates/sec
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Compugen Ltd.
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version =
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                                                       protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Perfect score:
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geneseqp2003as:* geneseqp2003bs:* geneseqp2000s:* geneseqp2001s:* geneseqp2004s:* geneseqp2002s:*

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

A_Geneseq_16Dec04:* geneseqp1980s:* geneseqp1990s:*

Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

		æ			SUMMAKIES	
Result No.	Score	Query Match	Length	DB	ID	Description
1	7.0	0	15	2	ABP52270	Abp52270 HLA-DR2
7	65	92.9	15	S	ABP52271	Abp52271 HLA-DR2
m	65	92.9	15	ß	ABP52272	Abp52272 HLA-DR2
4	65	92.9	15	ហ	ABP52298	Abp52298 HLA-DR2
ß	65	92.9	17	'n	ABP52294	Abp52294 HLA-DR2
9	65	92.9	17	Ŋ	ABP52296	Abp52296 HLA-DR2
7	65	92.9	19	ഹ	ABP52295	Abp52295 HLA-DR2
80	64	91.4	15	ß	ABP52257	_
თ	9	85.7	15	Ŋ	ABP52290	Abp52290 HLA-DR2
10	9	85.7	15	S	ABP52261	_
11	9	85.7	15	S	ABP52292	Abp52292 HLA-DR2
12	9	85.7	15	S	ABP52269	Abp52269 HLA-DR2
13	59	84.3	15	Ŋ	ABP52267	Abp52267 HLA-DR2
14	59	84.3	15	Ŋ	ABP52263	Abp52263 HLA-DR2
15	57	81.4	15	2	ABP52301	Abp52301 HLA-DR2
16	26	80.0	15	Ŋ	ABP52304	Abp52304 HLA-DR2
	26	80.0	17	'n	ABP52303	Abp52303 HLA-DR2
18	52	78.6	15	S	ABP52291	Abp52291 HLA-DR2
19	52		15	Ŋ	ABP52251	Abp52251 HLA-DR2
20		•	15	'n	ABP52248	Abp52248 HLA-DR2
21	52	78.6	15	S	ABP52268	Abp52268 HLA-DR2
22	55	•	15	Ŋ	ABP52239	Abp52239 HLA-DR2
23	54.5	77.9	15	ß	ABP52265	Abp52265 HLA-DR2
24	54	77.1	15	S	ABP52240	Abp52240 HLA-DR2

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abne2244 HI.a-DB2 m		HLA-	9 HLA-	Abp52262 HLA-DR2 m	Abp52260 HLA-DR2 m	Abp52305 HLA-DR2 m	Abp52302 HLA-DR2 m	Abp52255 HLA-DR2 m	Abp52253 HLA-DR2 m	Abp52242 HLA-DR2 m	Abp52297 HLA-DR2 m	Aay58969 Copeptide	8	Aag63198 Peptide w	9	Abp52289 HLA-DR2 m	Abp52266 HLA-DR2 m	Adj57542 Cop-1 rel	Add59601 Copolymer
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96	27	28	29	30	31	32	33	34	35	36	37	38	39		41	42	43	44	45

ALIGNMENTS

Human leukocyte antigen; HLA; major histocompatibility complex; MHC; HLA-DR2; MHC class II DR-2 molecule; demyelinating; multiple sclerosis; immune response; antiinflammatory; neuroprotective; proliferation; MHC class II protein inhibitor; demyelinating disease; inhibition; post-viral encephalomyelitis; post-vaccine demyelinating condition; anti-tumour necrosis factor agent. HLA-DR2 molecule binding peptide SEQ ID NO:64. ABPS2270 standard; peptide; 15 AA (first entry) Homo sapiens. 16-OCT-2002 Synthetic. ABP52270;

WO200259143-A2.

24-JAN-2002; 2002WO-US002071.

01-AUG-2002

24-JAN-2001; 2001US-0263569P

(HARD) HARVARD COLLEGE.

Ξ Strominger JL, Fridkis-Hareli

WPI; 2002-608439/65.

New compositions comprising synthetic peptides in complex with a major histocompatibility complex class II HLADR2 protein, useful for treating a demyelinating disease, e.g. multiple sclerosis, or post-viral encephalomyelitis.

Claim 28; Page 39; 54pp; English.

The present invention describes compositions (I) comprising a peptide with an amino acid sequence with tyrosine (Y), lysine (K), and/or valine residues. The complex of the peptide with a major histocompatibility complex (MHC) class II HLA-DR2 protein is involved in modulating an immune response. (I) has antiinflammatory and neuroprotective activities, and can be used as a MHC class II protein inhibitor. The compositions comprising the peptides are useful for treating demyelinating diseases

Abp52241 HLA-DR2

ABP52241

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Sequence 15 AA;

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The present invention describes compositions (1) comprising a peptide with an amino acid sequence with tyrosine (Y), lysine (K), and/or valine residues. The complex of the peptide with a major histocompatibility complex (MHC) class II HLA-DS protein is involved in modulating an immune response. (I) has antiinflammatory and neuroprotective activities, and can be used as AMC class II protein inhibitor. The compositions comprising the peptides are useful for treating demyelinating diseases such as multiple sclerosis, post-viral encephalomyelitis, a post-vaccine demyelinating condition, and a side effect of administering an antituour necrosis factor agents. The peptide further inhibits proliferation of autoantigen-specific HLA-DSR2-restricted I cell clones. ABP52207 to
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such as multiple sclerosis, post-viral encephalomyelitis, a post-vaccine demyelinating condition, and a side effect of administering an antimumur necrosis factor agents. The peptide further inhibits proliferation of autoantigen-specific HIA-DR2-restricted T cell clones. ABP52207 to
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human leukocyte antigen, HLA, major histocompatibility complex, MHC; HLA-DR2; MHC class II DR-2 molecule, demyelinating; multiple sclerosis; immune reepones, antiinflammatory, neuroprotective; proliferation; MHC class II protein inhibitor; demyelinating disease; inhibition; post-viral encephalomyelitis; post-vaccine demyelinating condition;
                                                                                                                                                                                                         Gaps
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0
                                                                                                                                                                Query Match
Best Local Similarity 100.0%; Pred. No. 8.6e-05;
Matches 15; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HLA-DR2 molecule binding peptide SEQ ID NO:65.
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                                                                                                                                     Sequence 15 AA;
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The present invention describes compositions (I) comprising a peptide with an amino acid sequence with tyrosine (Y), lysine (K), and/or valine residues. The complex of the peptide with a major histocompatibility complex (MEC) class II HAA-DE2 protein is involved in modulating an immune response. (I) has antiinflammatory and neuroprotective activities, and can be used as a MEC class II protein inhibitor. The compositions comprising the peptides are useful for treating demyelinating diseases such as multiple sclerosis, post-viral encephalomyelitis, a post-vaccine demyelinating condition, and a side effect of administering an antitumour necrosis factor agents. The peptide further inhibits proliferation of autcoantigen specific HAA-DRZ-restricted T cell clones. ABP52207 to ABP52305 represent peptides used in the exemplification of the present
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                                                                                                                                                                                                                                                                                                                 Human leukocyte antigen; HLA; major histocompatibility complex; MHC; HLA-DR2; MHC class II DR-2 molecule; demyelinating; multiple sclerosis; immune response; antiinflammatory; neuroprotective; proliferation; MHC class II protein inhibitor; demyelinating disease; inhibition; post-viral encephajomyelitis; post-vaccine demyelinating condition;
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Length 15;
                               1; Indels
Score 65; DB 5; I Pred. No. 0.00057;
                                                                                                                                                                                                                                                                                        HLA-DR2 molecule binding peptide SEQ ID NO:66.
                                   0; Mismatches
                                                                                                                                                                                         ABP52272 standard; peptide; 15 AA.
                                                                                                                                                                                                                                                                                                                                                                                                         anti-tumour necrosis factor agent
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     92.98;
                      93.3%;
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Best Local Similarity
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Synthetic.
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with an amino acid sequence with tyrosine (Y), jysine (K), and/or valine residues. The complex of the peptide with a major histocompatibility complex (MHC) class II HLA-DR2 brotein is involved in modulating an immune response. (I) has antihifammatory and neuroprotective activities, and can be used as a MHC class II protein inhibitor. The compositions comprising the peptides are useful for treating demyelinating diseases such as multiple sclerosis, post-viral encephalomyelitis, a post-vaccine demyelinating condition, and a side effect of administering an anti-tumour necrosis factor agents. The peptide further inhibits proliferation of antoantigen-specific HLA-DR2-resericted T cell clones. ABP52207 to ABP52305 represent peptides used in the exemplification of the present
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New compositions comprising synthetic peptides in complex with a major histocompatibility complex class II HLADR2 protein, useful for treating a demyelinating disease, e.g. multiple sclerosis, or post-viral encephalomyelitis.
                                                                                                                                                          Human leukocyte antigen; HLA; major histocompatibility complex; MHC; HLA-DR2; MHC class II DR-2 molecule; demyelinating; multiple sclerosis; immune response; antiinflammatory; neuroprotective; proliferation; MHC class II protein inhibitor; demyelinating disease; inhibition; post-viral encephalomyelitis; post-vaccine demyelinating condition; anti-tumour necrosis factor agent.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 present invention describes compositions (I) comprising a peptide
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Pred. No. 0.00057;
0; Mismatches 1; Indels
                                                                                                                      HLA-DR2 molecule binding peptide SEQ ID NO:92.
                ABP52298 standard; peptide; 15 AA
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Best Local Similarity 93.3%;
Matches 14; Conservative
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The present invention describes compositions (I) comprising a peptide with an amino acid sequence with tyrosine (Y), lysine (K), and/or value residues. The complex of the peptide with a major histocompatibility complex (MHC) class II HLA-DR2 protein is involved in modulating an immune response. (I) has antiinflammatory and neuroprotective activities, and can be used as a MHC class II protein inhibitor. The compositions comprising the peptides are useful for treating demyelinating diseases such as multiple sclerosis, post-viral encephalomyelitis, a post-vaccine demyelinating condition, and a side effect of administering an anti-tumour necrosis factor agents. The peptide further inhibits proliferation of autoantigen-specific HLA-DR2-restricted T cell clones. ABB52207 to ABB52305 represent peptides used in the exemplification of the present
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New compositions comprising synthetic peptides in complex with a major histocompatibility complex class II HLADR2 protein, useful for treating a demyelinating disease, e.g. multiple sclerosis, or post-viral encephalomyelitis.
                                                                                                       Human leukocyte antigen; HLA; major histocompatibility complex; MHC; HLA-DR2; MHC class II DR-2 molecule; demyelinating; multiple sclerosis; immune response; antinflammatory; neuroprotective; proliferation; MHC class II protein inhibitor; demyelinating disease; inhibition; post-viral encephalomyelitis; post-vaccine demyelinating condition;
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                                                                           HLA-DR2 molecule binding peptide SEQ ID NO:88.
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Pred. No. 0.000
0; Mismatches
                                                                                                                                                                                         anti-tumour necrosis factor agent
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                                                                                                                                                                                                                                                                                                                                                                                                                                    Strominger JL, Fridkis-Hareli M;
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ABP52294 standard; peptide; 17 AA.

ABP52294 ID ABP

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The present invention describes compositions (I) comprising a peptide with an amino acid sequence with tyrosine (Y), lysine (K), and/or valine residues. The complex of the peptide with a major histocompatibility complex (MHC) class II HLA-DE2 protein is involved in modulating an immune response. (I) has antiinflammatory and neuroprotective activities, and can be used as MHC class II protein inhibitor. The compositions comprising the peptides are useful for treating demyelinating diseases such as multiple sclerosis, post-viral encephalomyelitis, a post-vaccine tumour necrosis factor agents. The peptide further inhibits proliferation of autoantigen-specific HLA-DE2-restricted T cell clones ABB52207 to ABB52205 represent peptides used in the exemplification of the present
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Human leukocyte antigen, HLA, major histocompatibility complex; MHC, HLA-DR2; MHC class II DR-2 molecule; demyelinating; multiple sclerosis; immune response; antiinflammatory; neuroprotective; proliferation; MHC class II protein inhibitor; demyelinating disease; inhibition; post-viral encephalomyelitis; post-vaccine demyelinating condition; anti-tumour necrosis factor agent.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New compositions comprising synthetic peptides in complex with a major histocompatibility complex class II HLADR2 protein, useful for treating demyelinating disease, e.g. multiple sclerosis, or post-viral encephalomyelitis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 65; DB 5; Length 17;
Pred. No. 0.00065;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                            Fridkis-Hareli M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 28; Page 39; 54pp; English.
                                                                                                                                                                                                                                                                           24-JAN-2002; 2002WO-US002071.
                                                                                                                                                                                                                                                                                                               24-JAN-2001; 2001US-0263569P.
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                                                                                                                                                                                                                                                                                                                                                  (HARD ) HARVARD COLLEGE
                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2002-608439/65.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity
                                                                                                                                                                                             WO200259143-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 17 AA;
                                                                                                                                                                                                                                                                                                                                                                                          Strominger JL,
                                                                                                                                      Homo sapiens.
Synthetic.
                                                                                                                                                                                                                                     01-AUG-2002
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Best Local 9
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with an amino acid sequence with tyrosine (Y), lysine (K), and/or valine residues. The complex of the peptide with a major histocompatibility complex (MHC) class II HIA-DR2 protein is involved in modulating an immune response. (I) has antihiflammatory and neuroprotective activities, and can be used as a MHC class II protein inhibitor. The compositions comprising the peptides are useful for treating demelinating diseases such as multiple sclerosis, post-viral encephalomyelitis, a post-vaccine tumour necrosis factor agents. The peptide further inhibits proliferation of autoantigen specific HIA-DR2 respricted T cell clones. ABDF52307 to

Sequence 19 AA;

nvention.

present invention describes compositions (I) comprising a peptide

Claim 28; Page 39; 54pp; English.

encephalomyelitis.

New compositions comprising synthetic peptides in complex with a major histocompatibility complex class II HLADR2 protein, useful for treating demyelinating disease, e.g. multiple sclerosis, or post-viral

New compositions comprising

WPI; 2002-608439/65.

Ξ

Fridkis-Hareli

Strominger JL,

(HARD) HARVARD COLLEGE

24-JAN-2002; 2002WO-US002071 24-JAN-2001; 2001US-0263569P

WO200259143-A2

01-AUG-2002

Homo sapiens

Synthetic.

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                                                                                                                                                                                                                                                           Human leukocyte antigen, HLA, major histocompatibility complex, MHC, HLA-DR2; MHC class II DR-2 molecule, demyelinating, multiple sclerosis; immune responses; antiinflammacory, neuroprotective; proliferation; MHC class II protein inhibitor; demyelinating disease; inhibition; post-viral encephalomyelitis; post-vaccine demyelinating condition; anti-tumour necrosis factor agent.
                              Gaps
                              .
Score 65; DB 5; Length 19;
Pred. No. 0.00073;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                   HLA-DR2 molecule binding peptide SEQ ID NO:51.
                            0; Mismatches
                                                                                                                                                    ABP52257 standard; peptide; 15 AA.
ch 92.9%;
11 Similarity 93.3%;
14; Conservative
                                                        1 EAAKYEAYKAAAAA 15
                                                                        3 EKAKYEAYKAAAAA 17
                                                                                                                                                                                                        16-OCT-2002 (first entry)
              Best Local Similarity
Matches 14; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                  WO200259143-A2
                                                                                                                                                                                                                                                                                                                                                              sapiens
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  Query Match
                                                                                                                                    RESULT 8
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0; Gaps

Human leukocyte antigen, HLA, major histocompatibility complex; MHC, HLA-DR2; MHC class II DR-2 molecule; demyelinating; multiple sclerosis; immune response, antiinflammatory; neuroprotective; proliferation; MHC class II protein inhibitror; demyelinating disease; inhibition; post-viral encephalomyelitis; post-vaccine demyelinating condition; anti-tumour necrosis factor agent.

HLA-DR2 molecule binding peptide SEQ ID NO:89.

(first entry)

16-OCT-2002

ABP52295;

ABP52295 standard; peptide; 19 AA.

1 EAAKYEAYKAAAAA 15 EKAKYEAYKAAAAA 15

8 셤

14; Conservative

Matches

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with an amino acid sequence with tyrosine (Y), lysine (K), and/or valine residues. The complex of the peptide with a major histocompatibility complex (MHC) class II HLA-DE2 protein is involved in modulating an immune response. (I) has antiinflammatory and neuroprotective activities, and can be used as A MHC class II protein inhibitor. The compositions comprising the peptides are useful for treating demyelinating diseases such as multiple sclerosis, post-viral encephalomyelitis, a post-vaccine demyelinating condition, and a side effect of administering an anti-tumour necrosis factor agents. The peptide further inhibits proliferation of autoantigen-specific HLA-DR2-restricted T cell clones ABP52207 to
                                                                 New compositions comprising synthetic peptides in complex with a major histocompatibility complex class II HLADR2 protein, useful for treating a demyelinating disease, e.g. multiple sclerosis, or post-viral encephalomyelitis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ABP52305 represent peptides used in the exemplification of the present
                                                                                                                                                                                                                                    present invention describes compositions (I) comprising a peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 60; DB 5; Length 15;
Pred. No. 0.0037;
); Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HLA-DR2 molecule binding peptide SEQ ID NO:55.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ABP52261 standard; peptide; 15 AA.
                                                                                                                                                                                     Claim 28; Page 39; 54pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Strominger JL, Fridkis-Hareli M;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             85.7%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           13; Conservative
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                          WPI; 2002-608439/65.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 15 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         with an amino acid sequence with tyrosine (Y), lysine (K), and/or valine residues. The complex of the peptide with a major histocompatibility complex (HtC) class II HiA-DR2 protein is involved in modulating an immune response. (I) has antiinflammatory and neuroprotective activities, comprising the peptides are useful for treating demyelinating diseases such as multiple sclerosis, post-viral encephalomyelitis, a post-vaccine demyelinating condition, and a side effect of administering an anti-tumour necrosis factor agents. The peptide further inhibits proliferation of autoantigen-specific HiA-DR2-restricted T cell clones. ABB52207 to ABB52305 represent peptides used in the exemplification of the present
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                                                                                                                                                                                                                               New compositions comprising synthetic peptides in complex with a major histocompatibility complex class II HLADR2 protein, useful for treating demyelinating disease, e.g. multiple sclerosis, or post-viral
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human leukocyte antigen; HLA; major histocompatibility complex; MHC; HLA-DR2; MHC class II DR-2 molecule; demyelinating; multiple sclerosis; immune response; antiniflammatory; neuroprotective; proliferation; MHC class II protein inhibitor; demyelinating disease; inhibition; post-viral encephalomyelitis; post-vaccine demyelinating condition;
                                                                                                                                                                                                                                                                                                                                                                                            present invention describes compositions (I) comprising a peptide
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Pred. No. 0.00083;
); Mismatches 1; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Mismatches
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                                                                                                                                       Strominger JL, Fridkis-Hareli M;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ABP52290 standard; peptide; 15
24-JAN-2002; 2002WO-US002071,
                                           24-JAN-2001; 2001US-0263569P
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             91.4%;
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                                                                                         (HARD ) HARVARD COLLEGE
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                                                                                                                                                                              WPI; 2002-608439/65.
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                                                                                                                                                                                                                                                                                                     encephalomyelitis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 15 AA;
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Query Match Best Local S Matches

ABP52290;

RESULT 9

Homo

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Gaps

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immune response. (I) has antiinflammatory and neuroprotective activities, and can be used as MHC class II protein inhibitor. The compositions comprising the peptides are useful for treating demyelinating diseases such as multiple sclerosis, post-viral encephalomyelitis, a post-vaccine demyelinating condition, and a side effect of administering an antitumour necrosis factor agents. The peptide further inhibits proliferation of autoantigen-specific HIA-DEZ-restricted T cell clones, ABB52207 to ABB52305 represent peptides used in the exemplification of the present
                                                                                    with an amino acid sequence with tyrosine (Y), lysine (K), and/or valine residues. The complex of the peptide with a major histocompatibility complex (MHC) class II HLA-DR2 protein is involved in modulating an
                                                               present invention describes compositions (I) comprising a peptide
                       Example 1; Page 33; 54pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                               85.7%;
86.7%;
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EAAEYAAYKAAAAAA 15
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tes 13; Conservative
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                                                                                                                                                                                                                                                                                                                                         invention
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ABP52292
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HLA-DR2 molecule binding peptide SEQ ID NO:86. ABP52292 standard; peptide; 15 AA. (first entry) 16-OCT-2002

Human leukocyte antigen; HLA; major histocompatibility complex; MHC, HLA-DR2; MHC class II DR-2 molecule; demyelinating; multiple sclerosis; immune reaponse; antiinflammatory; neuroprotective; proliferation; MHC class II protein inhibitor; demyelinating disease; inhibition; post-viral encephalomyelitis; post-vaccine demyelinating condition; anti-tumour necrosis factor agent.

sapiens Homo

Synthetic

WO200259143-A2

01-AUG-2002.

24-JAN-2002; 2002WO-US002071

24-JAN-2001; 2001US-0263569P.

(HARD) HARVARD COLLEGE

Fridkis-Hareli M; Strominger JL,

WPI; 2002-608439/65.

New compositions comprising synthetic peptides in complex with a major histocompatibility complex class II HLADR2 protein, useful for treating a demyelinating disease, e.g. multiple sclerosis, or post-viral encephalomyelitis.

Claim 28; Page 39; 54pp; English.

The present invention describes compositions (I) comprising a peptide with an amino acid sequence with tyrosine (Y), lysine (K), and/or valine residues. The complex of the peptide with a major histocompatibility complex (MHC) class II HLA-DR2 protein is involved in modulating an

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immune response. (I) has antiinflammatory and neuroprotective activities, and can be used as AMC class II protein inhibitor. The compositions comprising the peptides are useful for treating demyelinating diseases such as multiple sclerosis, post-viral encephalomyelitis, a post-vaccine demyelinating condition, and a side effect of administering an anti-tumour necrosis factor agents. The peptide further inhibits proliferation of autoantigen-specific HLA-DRZ-restricted T cell clones, ABP552307 to ABP52305 represent peptides used in the exemplification of the present
                                                                                                                                                                                                                                                 invention
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Sequence 15 AA;

Gaps ; 0 Length 15; Score 60; DB 5; Length 15; Pred. No. 0.0037; 0; Mismatches 2; Indels 85.78; Query Match
Best Local Similarity 86.7
Matches 13; Conservative

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RESULT 12

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0; Gaps

Score 60; DB 5; Length 15; Pred. No. 0.0037; 1; Mismatches 1; Indels

1; Mismatches

ABP52269 standard; peptide; 15 AA.

ABP52269;

16-OCT-2002 (first entry)

HLA-DR2 molecule binding peptide SEQ ID NO:63.

Human leukocyte antigen; HLA; major histocompatibility complex; MHC; HLA-DR2; MHC class II DR-2 molecule; demyelinating; multiple sclerosis; immune response; antiinflammatory; neuroprotective; proliferation; MHC class II protein inhibitor; demyelinating disease; inhibition; post-viral encephalomyelitis; post-vaccine demyelinating condition; anti-tumour necrosis factor agent.

sapiens. Synthetic. Homo

WO200259143-A2.

01-AUG-2002

24-JAN-2002; 2002WO-US002071.

24-JAN-2001; 2001US-0263569P.

(HARD) HARVARD COLLEGE

Strominger JL, Fridkis-Hareli M;

WPI; 2002-608439/65.

New compositions comprising synthetic peptides in complex with a major histocompatibility complex class II HLADR2 protein, useful for treating a demyelinating disease, e.g. multiple sclerosis, or post-viral encephalomyelitis.

Claim 28; Page 39; 54pp; English.

The present invention describes compositions (I) comprising a peptide with an amino acid sequence with tyrosine (Y), lysine (K), and/or valine residues. The complex of the peptide with a major histocompatibility complex (MHC) class II HIA-DR2 protein is involved in modulating an immune response. (I) has antiinflammatory and neuroprotective activities, and can be used as A MHC class II protein inhibitor. The compositions comprising the peptides are useful for treating demyelinating diseases such as multiple sclerosis, post-viral encephalomyelitis, a post-vaccine demyelinating condition, and a side effect of administering an antitumour necrosis factor agents. The peptide further inhibits proliferation of autoantigen-specific HIA-DR2-restricted T cell clones. ABP52207 to

Gaps

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Indels

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Mismatches

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15

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1 EAAKYEAYKAAAAA
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      13; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New compositions comprising synthetic peptides in complex with a major histocompatibility complex class II HLADR2 protein, useful for treating demyelinating disease, e.g. multiple sclerosis, or post-viral encephalomyelitis.
                                                                                                                                                                                                                                                                                              Human leukocyte antigen; HLA; major histocompatibility complex; MHC; HLA-DR2; MHC class II DR-2 molecule; demyelinating; multiple sclerosis; immune response; antiinflammatory; neuroprotective; proliferation; MHC class II protein inhibitor; demyelinating disease; inhibition; post-viral encephalomyelitis; post-vaccine demyelinating condition;
represent peptides used in the exemplification of the present
                                                                                        Gaps
                                                                                       ;
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                                                           85.7%; Score 60; DB 5; Length 15; 86.7%; Pred. No. 0.0037; 1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                        HLA-DR2 molecule binding peptide SEQ ID NO:61.
                                                                                                                                                                                                ABP52267 standard; peptide; 15 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         24-JAN-2002; 2002WO-US002071
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                                                                                                                        ||| |:||||||||
EAAAYKAYKAAAAA 15
                                                                                                             1 EAAKYEAYKAAAAA 15
                                                                                                                                                                                                                                                 (first entry)
                                                                       Local Similarity 86.7 es 13; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (HARD ) HARVARD COLLEGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2002-608439/65.
                                     Sequence 15 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                        WO200259143-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 15 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Strominger JL,
                                                                                                                                                                                                                                                                                                                                                                                       sapiens.
                                                                                                                                                                                                                                                 16-OCT-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                01-AUG-2002
                                                                                                                                                                                                                                                                                                                                                                                                  Synthetic.
              nvention
                                                                                                                                                                                                                         ABP52267;
                                                             Query Match
                                                                          Best Loca
Matches
                                                                                                                                                                                                                                                                                                                                                                                       Homo
                                                                                                                                                                         RESULT 13
                                                                                                                                                                                   ABP52267
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Score 59; DB 5; Length 15; Pred. No. 0.0055;

84.38;

Query Match Best Local Similarity

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                with an amino acid sequence with tyrosine (X), jusine (K), and/or valine residues. The complex of the peptide with a major histocompatibility complex (MtC) class II MLA-DR2 protein is involved in modulating an immune response. (I) has antiinflammatory and neuroprotective activities, and can be used as a MtC class II protein inhibitor. The compositions comprising the peptides are useful for treating demyelinating diseases such as multiple sclerosis, post-viral encephalomyelitis, a post-vacine demyelinating condition, and a side effect of administering an anti-tumour necrosis factor agents. The peptide further inhibits proliferation of autocantigen-specific HLA-DR2-restricted T cell clones. ABB52207 to ABB52305 represent peptides used in the exemplification of the present
                                                                                                                                                                                                                                                                                     Human leukocyte antigen; HLA; major histocompatibility complex; MHC; HLA-DR2; MHC class II DR-2 molecule; demyelinating; multiple sclerosis; immune response; antinflammatory; neuroprotective; proliferation; MHC class II protein inhibitor; demyelinating disease; inhibition; post-viral encephalomyelitis; post-vaccine demyelinating condition;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The present invention describes compositions (I) comprising a peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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86.7%; Pred. No. 0.0055;
ive 0; Mismatches 2; Indel8
                                                                                                                                                                                                              HLA-DR2 molecule binding peptide SEQ ID NO:57.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Example 1; Page 33; 54pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         anti-tumour necrosis factor agent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Strominger JL, Fridkis-Hareli M;
ABP52263 standard; peptide; 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            24-JAN-2001; 2001US-0263569P.
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                                                                                                                                          (first entry)
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                                                                                                                                          16-OCT-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Synthetic.
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The present invention describes compositions (1) comprising a peptide with an amino acid sequence with tyrosine (Y), lysine (K), and/or valine residues. The complex of the peptide with a major histocompatibility complex (MHC) class II HLA-DE protein is involved in modulating an immune response. (1) has antiinflammatory and neuroprotective activities, and can be used as MHC class II protein inhibitor. The compositions comprising the peptides are useful for treating demyelinating diseases such as multiple sclerosis, post-viral encephalomyelitis, a post-vaccine demyelinating condition, and a side effect of administering an antitumour necrosis factor agents. The peptide further inhibits proliferation of autoantigen-specific HLA-DES. restricted T cell clones. ABP52207 to ABP52305 represent peptides used in the exemplification of the present
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New compositions comprising synthetic peptides in complex with a major histocompastibility complex class II HLADR2 protein, useful for treating a demyelinating disease, e.g. multiple sclerosis, or post-viral encephalomyelitis.
                                                                                                                                                                                                                                                                                                                                                Human leukocyte antigen; HLA; major histocompatibility complex; MHC; HLA-DR2; MHC class II DR-2 molecule; demyelinating; multiple sclerosis; immune response; antiinflammatory; neuroprotective; proliferation; MHC class II protein inhibitor; demyelinating disease; inhibition; post-viral encephalomyelitis; post-vaccine demyelinating condition;
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80.0%; Pred. No. 0.012;
tive 2; Mismatches 1; Indels
                                                                                                                                                                                                                                                                              HLA-DR2 molecule binding peptide SEQ ID NO:95.
                                         ABP52301 standard; peptide; 15 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             anti-tumour necrosis factor agent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Strominger JL, Fridkis-Hareli M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 28; Page 39; 54pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                24-JAN-2001; 2001US-0263569P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      24-JAN-2002; 2002WO-US002071
                                                                                                                                                                                                     (first entry)
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Best Local Similarity 80.0
Matches 12; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2002-608439/65.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WO200259143-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens.
                                                                                                                                                                                                16-OCT-2002
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                                                                                                                           ABP52301;
ABP52301
ABP ABP52301
XXX
AC ABP
XXX
ADP 16-
XXX
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ADP 16-
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Gaps ö

Search completed: March 31, 2005, 02:35:27 Job time : 89.7903 secs

1 EAAKYEAYKAAAAA 15 | ||:||:||:|||||| EKAKFEAFKAAAAA 15

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
                                                                                                                   OM protein - protein search, using sw model
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March 31, 2005, 02:26:53 ; Search time 22.9839 Seconds (without alignments) 48.718 Million cell updates/sec Run on:

US-10-056-583A-64 70 Title: Perfect score:

1 EAAKYEAYKAAAAA 15 Sequence: BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

513545 seqs, 74649064 residues Searched:

513545 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

/cgn2_6/ptodata/1/iaa/5A_COMB.pep:*
/cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
/cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
/cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
/cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
/cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:* Issued_Patents_AA:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

		di			SUMMARIES		
Result No.	Score	Query Match	Length	DB	ID	Description	
-	42	60.0		'n	PCT-US95-04121-38	Sequence 38, Appl	
8	40	57.1	13	S	PCT-US94-10257A-33	33,	
m	40	57.1	391	4	US-09-902-540-11110		
4	40	57.1	466	4	US-09-489-039A-13950	Sequence 13950, A	
S	39.5	56.4	21	-	US-07-988-754-4		
9	39.5	56.4	33	-1	US-07-988-754-12		
7	39	55.7	186	4	US-09-902-540-11242		
æ		55.7	296	7	US-08-836-620A-16		
6	39	55.7	601	4	US-09-252-991A-21824	2182	
10	39	55.7	731	4	US-09-252-991A-18769	Sequence 18769, A	
11	38.5	55.0	98	4	US-09-405-743A-6		
12	38.5	55.0	98	4	US-09-816-989A-6	9	
13	38	54.3	64	4	US-09-248-796A-26627		
14	38	54.3	407	4	US-09-252-991A-29581	Sequence 29581, A	
15	38	54.3	ß	4	US-09-252-991A-32086	m	
16	37	52.9	20	H	US-08-440-861-23		
17	37	52.9		9	5169933-42		
18	. 37	52.9	25	9	5169933-42	Patent No. 5169933	
19	37	52.9	109	4	US-09-405-743A-7	Sequence 7, Appli	
20	37	52.9	109	4	US-09-816-989A-7	7,	
21	37	52.9	301	-	US-08-440-861-2	'n	
22	37	52.9	301	-4	US-08-433-854-2	~	
23	37	52.9	301	Н	US-08-174-745A-2	ď	
24	37	52.9		7	US-08-195-947-2	'n	
25	37	52.9		~	US-08-433-885-2	'n	
56	37	52.9	301	N	US-08-433-908B-2	Sequence 2, Appli	
27	37	52.9		m	US-08-410-614-2	7	

Seguence 46186, A	48,	Sequence 2, Appli	Sequence 3940, Ap	Sequence 4256, Ap	Sequence 5116, Ap	Sequence 6, Appli	Sequence 6, Appli	Sequence 4, Appli	Sequence 11230, A	Sequence 18658, A	Sequence 11523, A	Sequence 11524, A	Sequence 60, Appl	Sequence 42, Appl	Sequence 2, Appli	Sequence 2, Appli
US-09-270-767-46186	US-09-536-784-48	US-09-196-857-2	US-09-583-110-3940	US-09-107-433-4256	US-09-543-681A-5116	US-08-295-670-6	US-08-633-485-6	US-08-508-761B-4	US-09-489-039A-11230	US-09-248-796A-18658	US-09-949-016-11523	US-09-949-016-11524	PCT-US95-04121-60	US-09-117-121-42	US-09-405-743A-2	US-09-816-989A-2
4 r	4	m	4	4	4	Н	Н	٣	4	4	4	4	S	m	4	4
400	426	427	427	435	459	497	497	510	802	1001	741	741	13	37	45	45
52.9	52.9	52.9	52.9	52.9	52.9	52.9	52.9	52.9	52.9	52.9	52.1	52.1	51.4	51.4	51.4	51.4
37	37	37	37	37	37	37	37	37	37	37	36.5	36.5	36	36	36	36
28 24 26	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

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Gaps
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0
                                                                                                  TITLE OF INVENTION: Haptenated Peptides and Uses Thereof NUMBER OF SEQUENCES: 62
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/04121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2; Indels
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Pred. No. 0.82;
1; Mismatches
                                  Sequence 38, Application PC/TUS9504121; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                  CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/222,206
FILING DATE: April 1, 1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: Vanstone, Darlene A.
REGISTRATION NUMBER: 35,279
REFERENCE/DOCKET NUMBER: 075
TELECOMMUNICATION: TELEPHONE: (617) 466-6000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEFAX: (617) 466-6010
INFORMATION FOR SEQ ID NO: 38:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 60.0%;
Best Local Similarity 76.9%;
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 13 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE: peptide
FRAGMENT TYPE: internal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    amino acid
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TELEFAX: (
RESULT 1
PCT-US95-04121-38
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PCT-US94-10257A-33; Sequence 33, Application PC/TUS9410257A; GENERAL INFORMATION: APPLICANT: IMMULOGIC PHARMACEUTICAL CORPORATION:

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APPLICANT: Gary Breton et. al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
TITLE OF INVENTION: PIREMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: PIREMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
CURRENT APPLICATION NUMBER: US/09/489,039A
CURRENT FILING DATE: 1090-01-27
PRIOR FILING DATE: 1999-01-29
NUMBER OF SEQ ID NOS: 14342
SEQ ID NO 13950
LENGTH: 466
                                                         Gaps
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    Score 40; DB 4; Length 391;
Pred. No. 59;
3; Mismatches 4; Indels
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ZIP: 01748
COUNTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION NUMBER: US/07/988,754
FILING DATE: 19921210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 40; DB 4
Pred. No. 71;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
APPLICANT: Pang, Koy H.L.
APPLICANT: Cohen, Charles M.
APPLICANT: Keck, Peter C.
TITLE OF INVENTION: Synthetic Bioadhesive
UNDBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/627,323
FILING DATE: 14-DEC-1990
ATTORNEY/AGENT INFORMATION:
REGISTRATION NUMBER: 32,743
REPERENCE/DOCKET NUMBER: 32,743
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                            Sequence 13950, Application US/09489039A Patent No. 6610836
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE: Creative Biomolecules
STREET: 35 South Street
CITY: Hopkinton
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 4, Application US/07988754 Patent No. 5374431
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: PRT
ORGANISM: Klebsiella pneumoniae
       Query Match 57.1%;
Best Local Similarity 53.3%;
Matches 8; Conservative
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76.9%;
                                                                                                  1 EAAKYEAYKAAAAA 15
                                                                                                                            153 ASLEAQKAAAAA 165
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Best Local Similarity 76.9
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
                                                                                                                                                                                                                                           US-09-489-039A-13950
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US-07-988-754-4
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APPLICANT: BRIGITTE DEVAUX

APPLICANT: JONATHAN B. ROTHBARD

APPLICANT: DAWN SHLEK

APPLICANT: DAWN SHLEK

TITLE OF INVENTION: GLYCOPROTEIN AND PEPTIDE PORTIONS THEREOF IN PROTOCOLS

TITLE OF INVENTION: RELATED TO AUTOIMMUNE DISEASE

NUMBER OF SEQUENCES: 95

CORRESPONDENCE ADDRESS:

ADDRESSEE: IMMULOGIC PHARMACEUTICAL CORPORATION

STREET: 610 LINCOLN STREET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-09-902-540-11110

; Sequence 11110, Application US/09902540
; Patent No. 6813447
; GENERAL INFORMATION:
; APPLICANT: Goldman, Barry S.
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Wiegand, Roger C.
; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof; FILE REFERENCE: 38-10(1549)B
; CURRENT FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: 60/217,883
; FILING DATE: 2000-07-10
; NUMBER OF SEQ ID NOS: 16825
; SEQ ID NO 11110
; LEWORTH: 391
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 40; DB 5
Pred. No. 1.7;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US 08/116,824
FILING DATE: 03-SEP-1993
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: ANNE I CRAIG
REGISTRATION NUMBER: 32,976
REFERENCE/DOCKET NUMBER: 071.1 PCT
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION: (617) 466-6040
TELEFAX: (617) 466-6040
                                                                                                                                                                                                                                                                                                    ZIP: 02145
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCIT text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/10257A
FILING DATE: 1 SEPTEMBER 1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    57.1%;
76.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM: Myxococcus xanthus US-09-902-540-11110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 13 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 76.9
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3 AKYEAYKAAAAA 15
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                                                                                                                                                                                                                                    CITY: WALTHAM
STATE: Massachusetts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: amino acid
STRANDEDNESS: sin
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                    USA
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PCT-US94-10257A-33
                                                                                                                                                                                                                                                                                    COUNTRY:
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FILING DATE: 15-MAR-1996
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: GB 9607532.0
FILING DATE: 11-APR-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9609576.5
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   55.7%; Score 39;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/EP96/03933
FILING DATE:
APPLICATION NUMBER: GB 9518272.1
FILING DATE: 08-58P1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9605550.4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/836,620A
                                                                        Sequence 11242, Application US/09902540 Patent No. 6833447
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT:
TITLE OF INVENTION: Orphan receptor
NUMBER OF SEQUENCES: 19
COMPUTER READABLE FORM:
MEDIUM TYBE: Floppy disk
COMPUTER: IBM PC COMPALIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Orphan receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: GB 9609576.5
FILING DATE: 08-MAY-1996
INFORMATION FOR SEQ ID NO: 16:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 16, Application US/08836620A
Patent No. 5958710
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                     55.7%;
                                                                                                                                                                                                                                                                                                                                                                               ; ORGANISM: Myxococcus xanthus US-09-902-540-11242
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amino acid
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Best Local Similarity 61...
Best Local Similarity 61...
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48 SASYQKYKAAADA 60
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ORGANISM: Rai
                                                           JS-09-902-540-11242
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                                                                                                                                                                                                                                   56.4%; Score 39.5; DB 1; Length 21; 68.8%; Pred. No. 3.4;
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                                                                                                                                                                                                                                                                        Indels
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APPLICANT: Cohen, Charles M.
APPLICANT: Keck, Peter C.
TITLE OF INVENTION: Synthetic Bioadhesive
CORRESPONDENCES: 12
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION: 53.0
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/627,323
FILING DATE: 14-DEC-1990
ATTORNEY/AGENT INFORMATION:
NAME: LUNN, Paul G.
REGISTRATION NUMBER: 32,743
REFERENCE/DOCKET NUMBER: 22,743
RECOMMUNICATION INFORMATION:
TELEPHONE: (508) 435-9001
TELEPHONE: (508) 435-9001
TELEPHONE: (508) 435-6951
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 33 anino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE: Creative Biomolecules
STREET: 35 South Street
CITY: Hopkinton
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           56.4%;
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TELEPAX: (508) 435-6951
INFORMATION FOR ESO ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 21 amino acids
TYPE: AMINO ACID
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
                                                                                                                                                                             ; FRAGMENT TYPE: N-terminal US-07-988-754-4
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Best Local Similarity 68.8
Matches 11, Conservative
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Matches 11; Conservative
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US-07-988-754-12
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GENERAL INFORMATION:
APPLICANT: Goldman, Barry S.
APPLICANT: Hinkle, Gregory J.
APPLICANT: Stater, Steven C.
APPLICANT: Wiegand, Roger C.
TITLE OF INVENTION: Myxcoccus xanthus Genome Sequences and Uses Thereof FILE REFERENCE: 38-10 (15849)B
CURRENT APPLICATION NUMBER: US/09/902,540
CURRENT APPLICATION NUMBER: 60/217,883
PRIOR APPLICATION NUMBER: 60/217,883
PRIOR FILING DATE: 2000-07-10
NUMBER OF SEQ ID NOS: 16825
SEQ ID NO 11442
LENGTH: 186 Gaps ö Score 39; DB 4; Length 186; Pred. No. 40; 2; Mismatches 3; Indels DB 2; Length 596; SOFTWARE: PatentIn Release #1.0, Version #1.25 (BPO)

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APPLICANT: Lis, Doris
TITLE OF INVENTION: COPOLYMER I RELATED POLYPEPTIDES FOR USE AS MOLECULAR WEIGHT MARKI
TITLE OF INVENTION: COPOLYMER I RELATED POLYPEPTIDES FOR USE AS MOLECULAR WEIGHT MARKI
TITLE OF INVENTION: AND FOR THERAPEUTIC USE
FILE OF INVENTION: AND FOR THERAPEUTIC USE
CURRENT APPLICATION NUMBER: US/09/816,989A
CURRENT APPLICATION NUMBER: 00/101,693
PRIOR APPLICATION NUMBER: 60/101,693
PRIOR APPLICATION NUMBER: PC/US99/22402
PRIOR PILING DATE: 1999-09-24
NUMBER OF SEQ ID NOS: 7
SEQ ID NO 6
LENGTH: 86
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Patent No. 6747137
GENERAL INFORMATION:
GENERAL THORMATION:
APPLICANT: Keith Weinstock et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICANS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; OTHER INFORMATION: Description of Artificial Sequence: Synthetic Peptide US-09-816-989A-6
                                                                                                                    GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Yeda Research and Development Co., Ltd.
TITLE OF INVENTION: GLATIRAMER ACETATE MOLECULAR WEIGHT MARKERS
FILE REFERENCE: 60807-A
CURRENT APPLICATION NUMBER: US/09/405,743A
CURRENT FILING DATE: 1999-09-24
NUMBER OF SEQ ID NOS: 7
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 6
LENGTH: 86
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4; Length 86,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                       OTHER INFORMATION: Description of Artificial Sequence: OTHER INFORMATION: PEPTIDE
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Pred. No. 22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1; Mismatches
                                                                           Sequence 6, Application US/09405743A Patent No. 6514938
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          55.0%;
73.3%;
                                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM: Artificial Sequence FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: PRT ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 EAAKYEAYKAAAAA 15
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Best Local Similarity 73.33
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
APPLICANT: Gad, Alexander
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 13
US-09-248-796A-26627
                                                      US-09-405-743A-6
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US-09-816-989A-6
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                                                                                                                                                                                                                                    Sequence 21824, Application US/09252991A

Patent No. 6551795
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REPRENCATION WURBER: US 609/252,991A

CURRENT APPLICATION NUMBER: US 60/074,788
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR SEQ ID NOS: 33142

SEQ ID NO 21824

LENGTH: 601
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Batent No. 6551795
GENERAL INCOMPATION:
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
TITLE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR FILING DATE: 1998-02-18
PRIOR FILING DATE: 1998-02-18
PRIOR FILING DATE: 1998-02-18
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 18769
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; OTHER INFORMATION: Identity of amino acid at the above locations are unknown. US-09-252-991A-21824
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
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                            Gaps
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Pred. No. 1.3e+02;
3; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         55.7%; Score 39; DB 4; Length 731; 72.7%; Pred. No. 1.7e+02; ive 1; Mismatches 2; Indels
                            Indels
  Pred. No. 1.3e+02;
0; Mismatches 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM: Pseudomonas aeruginosa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM: Pseudomonas aeruginosa
Best Local Similarity 66.7%;
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 58.3%;
Matches 7; Conservative
                                                                        1 EAAKYEAYKAAAAA 15
                                                                                                                          56 EGAAYEFNAAAAAA 70
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179 YEAYEAACARA 189
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Best Local Similarity
Matches 8; Conserv
                                                                                                                                                                                                  RESULT 9
US-09-252-991A-21824
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Sequence 29581, Application US/09252991A

Sequence 29581, Application US/09252991A

Patent No. 6551795

GENERAL INFORMATION:

APPLICANT: Marc J. Rubenfield et al.

TITLE OF INVENTION: ARRUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS

TITLE OF INVENTION: ARRUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS

TITLE OF INVENTION: ARRUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS

FILE REFERENCE: 107196.136

CURRENT APPLICATION NUMBER: US 60/074,788

PRIOR PILING DATE: 1999-02-18

PRIOR PLING DATE: 1998-02-18

PRIOR PLING DATE: 1998-02-18

PRIOR PLING DATE: 1998-02-18

SEQ ID NO 29581

SEQ ID NO 29581

LENGTH: 407
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Batent No. 6551795
GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AERGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REPERENCE: 107196.18
CURRENT APPLICATION NUMBER: US 60/074,788
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR FILING DATE: 1998-02-18
PRIOR FILING DATE: 1998-02-18
PRIOR SPLICATION NUMBER: US 60/094,190
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 32086
LENGTH: 534
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                                                                                                                                                                                                                                                                                                                                                                     Score 38; DB 4; Length 64; Pred. No. 19;
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FOR DIAGNOSTICS AND THERAPEUTICS
                                                                                                                                                                                                                                                                                                                                                                                                                     0; Mismatches
                                                | PRIOR APPLICATION NUMBER: US 0/09/248,796A | PRIOR APPLICATION NUMBER: US 60/074,725 | PRIOR FILING DATE: 1998-02-13 | PRIOR APPLICATION NUMBER: US 60/096,409 | PRIOR FILING DATE: 1998-08-13 | NUMBER OF SEQ ID NOS: 28208 | SEQ ID NO 26627 | LENGTH: 64
                    FILE REFERENCE: 107196.132
CURRENT APPLICATION NUMBER: US/09/248,796A
CURRENT FILING DATE: 1999-02-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-29581
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Best Local Similarity 71.4%;
Matches 10; Conservative
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263 EAAKKKAAAAAAA 276
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                                                                                                                                                                                                                                                                 TYPE: PRT ORGANISM: Candida albicans
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Best Local Similarity 71.43
Matches 10; Conservative
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US-09-252-991A-32086
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                                                                                       Length 534;
                                                                                 Query Match 54.3%; Score 38; DB 4; Length 534 Best Local Similarity 64.3%; Pred. No. 1.7e+02; Matches 9; Conservative 2; Mismatches 3; Indels
TYPE: PRT
ORGANISM: Pseudomonas aeruginosa
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332 EAAHVEAHRADAAA 345
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                                        US-09-252-991A-32086
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Copyright (c) 1993 - 2005 Compugen Ltd.
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Maximum Match 100%
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Maximum DB seq length: 200000000
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Perfect score:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

		:	Appl												
		_	64,	65,	99	88,	90,	89,	51,	55,	63,	84,	86,	57,	61,
	-	Description	Sequence	Seguence	Seguence	Seguence	Sequence	Seguence	Sequence	Seguence	Sequence	Seguence	Seguence	Sequence	Sequence
OCT TATELLING		qi	US-10-056-583-64	US-10-056-583-65	US-10-056-583-66	US-10-056-583-88	US-10-056-583-90	US-10-056-583-89	US-10-056-583-51	US-10-056-583-55	US-10-056-583-63	US-10-056-583-84	US-10-056-583-86	US-10-056-583-57	US-10-056-583-61
		- 1	14	14	14	14	14	14	14	14	14	14	14	14	14
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		Score	70	65	65	65	65	65	64	9	9	9	9	59	59
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100.0%; Score 70; DB 14; Length 15; 100.0%; Pred. No. 9e-05; tive 0; Mismatches 0; Indels

Query Match Best Local Similarity 100.0 Matches 15; Conservative 1 EAAKYEAYKAAAAA 15 |||||||||||||| 1 EAAKYEAYKAAAAA 15

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RESULT 2 US-10-056-583-65

Sequence 95, Appl Sequence 92, Appl Sequence 97, Appl Sequence 33, Appl Sequence 42, Appl Sequence 62, Appl Sequence 62, Appl Sequence 85, Appl Sequence 34, Appl Sequence 34, Appl Sequence 34, Appl Sequence 35, Appl Sequence 35, Appl Sequence 37, Appl	. 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4	ege ELINATING Synthesized.
0.056 - 583 - 0.056 - 0.056 -	10 0 0 56 5 58 3 5 5 10 0 0 56 5 58 3 5 10 0 0 56 5 58 5 10 0 0 0 56 5 58 5 10 0 0 0 56 5 58 5 10 0 0 0 56	ALIGNMENTS Of Harvard Coll EPTIDES FOR DEMY /056,583 569 sion 4.0
1155 1155 1155 1155 1155 1155 1155 115		nn US/10056 1064915A1 and Fellow , Jack L. Traeli, Mash ERAPEUTIC CONDITIONS 017 2002-01-24 ER: 60/263 99 Windows Ve Sequence
24 4 4 5 5 5 5 5 6 6 6 7 7 7 7 7 8 8 8 8 8 8 8 8 8 8 8 8	553 553 553 553 553 553 553 553 553 553	-583-64 e 64, Applicatio tion No. US20030 INPORMATION: ANT: Presidents ANT: Strominger ANT: Strominger ANT: Strominger ANT: Frickis-Ha ANT: Frickis-Ha ANT: Frickis-Ha ANT: Frickis-Ha ANT: Frickis-Ha ANT: Frickis-Ha EFRERENCE: 24655- EFRERENCE: 24655- EFRERENCE: 24655- EFILING DATE: APPLICATION NUMB FILING DATE: 200 FRE: FASTSEQ for NO 64 H: 15 PRT INFORMATION: Th -583-64
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; APPLICANT: Fridkis-Hareli, Masha; ITTLE OF INVENTION: THERAPEUTIC PEPTIDES FOR DEMYELINATING; TITLE OF INVENTION: THERAPEUTIC PEPTIDES FOR DEMYELINATING; TITLE OF INVENTION: CONDITIONS; FILE REPRENCE: 2655-017; CURRENT PILING DATE: 2002-01-24; PRIOR APPLICATION NUMBER: 60/263,569; PRIOR APPLICATION NUMBER: 60/263,569; PRIOR PILING DATE: 2001-01-24; NUMBER OF SEQ ID NOS: 99; SOPTWARR: FASTERQ for Windows Version 4.0; SEQ ID NO 88; LENGTH: 17
                                                                                                                                                                                                                                                                                                                                                                                             FEATURE:
; OTHER INFORMATION: The peptide was designed and synthesized
US-10-056-583-88
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US-10-056-583-90
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; Sequence 90, Application US/10056583
; Publication No. US20030064915A1
; GENERAL INFORMATION:
; APPLICANT: Presidents and Fellows of Harvard College
; APPLICANT: Strominger, Jack L.
; APPLICANT: Fridkis-Hareli, Masha
; TITLE OF INVENTION: THERAPEUTIC PEPTIDES FOR DEMYELINATING
; TITLE OF INVENTION: CONDITIONS
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Publication No. US20030064915A1
GENERAL INFORMATION:
APPLICANT: Presidents and Fellows of Harvard College
APPLICANT: Strominger, Jack L.
APPLICANT: Fridkis-Hareli, Masha
TITLE OF INVENTION: THERAPEUTIC PEPTIDES FOR DEMYELINATING
TITLE OF INVENTION: CONDITIONS
FILE REFERENCE: 24655-017
CURRENT APPLICATION NUMBER: US/10/056,583
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 92.9%; Score 65; DB 14;
Best Local Similarity 93.3%; Pred. No. 0.00066;
Matches 14; Conservative 0; Mismatches 1;
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92.9%; Score 65; DB 14;
Best Local Similarity 93.3%; Pred. No. 0.00066;
Matches 14; Conservative 0; Mismatches 1.
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CURRENT APPLICATION NUMBER: US/10/056,583
CURRENT FILING DATE: 2002-01-24
PRIOR APPLICATION NUMBER: 60/263,569
PRIOR FILING DATE: 2001-01-24
NUMBER OF SEQ ID NOS: 99
SOFTWARE: PastSEQ for Windows Version 4.0
SLENGTH: 17
                                                                                                                                                                                                                                                                                                                                                                      ORGANISM: Artificial Sequence
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ORGANISM: Artificial Sequence
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                                                                     GENERAL INFORMATION:

APPLICANT: Presidents and Fellows of Harvard College
APPLICANT: Strominger, Jack L.

APPLICANT: Strominger, Jack L.

APPLICANT: Strominger, Jack L.

TITLE OF INVENTION: THERAPEUTIC PEPTIDES FOR DEMYELINATING
TITLE OF INVENTION: CONDITIONS

FILE REFERENCE: 24655-017

CURRENT PELLOATION NUMBER: 60/263,569

PRIOR APPLICATION NUMBER: 60/263,569

PRIOR APPLICATION NUMBER: 60/263,569

PRIOR APPLICATION NUMBER: 60/263,569

NUMBER OF SEQ ID NOS: 99

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 65

LENTH: 15

TYPE: PRT

ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-10-056-583-66;

Sequence 66, Application US/10056583

Sequence 66, Application US/10056583

Publication No. US20030064915A1

GENERAL INFORMATION:
APPLICANT: Presidents and Fellows of Harvard College
APPLICANT: FirdMis-Harell, Masha
TITLE OF INVENTION: THERAPEUTIC PEPTIDES FOR DEMYELINATING
FILE OF INVENTION: CONDITIONS
FILE REPERENCE: 24655-017

CURRENT APPLICATION NUMBER: US/10/056,583

CURRENT FILING DATE: 2002-01-24

PRIOR PILING DATE: 2001-01-24

PRIOR PILING DATE: 2001-01-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OTHER INFORMATION: The peptide was designed and synthesized
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OTHER INFORMATION: The peptide was designed and synthesized
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 92.9%; Score 65; DB 14; Length 15; Best Local Similarity 93.3%; Pred. No. 0.00058; Matches 14; Conservative 0; Mismatches 1; Indels
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 66
LENGTH: 15
  Sequence 65, Application US/10056583
Publication No. US20030064915A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM: Artificial Sequence
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US-10-056-583-88
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Gaps

FEATURE:

Matches

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Gaps

Gaps

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Sequence 84, Application US/10056583

Sequence 84, Application US/10056583

Publication No. US20030064915A1

GENERAL INFORMATION:

APPLICANT: Presidents and Fellows of Harvard College
APPLICANT: Strominger, Jack L.

APPLICANT: Pridkis-Hareli, Masha

ITILE OF INVENTION: CONDITIONS

FILE REFERENCE: 24655-017

CURRENT APPLICATION NUMBER: US/10/056,583

CURRENT APPLICATION NUMBER: 08/10/056,583

FILE REPLATION DATE: 2001-01-24

PRIOR FILING DATE: 2001-01-24

NUMBER OF SEQ ID NOS: 99

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 84

LENGTH: 15
                                                                                                                          ; OTHER INFORMATION: The peptide was designed and synthesized US-10-056-583-55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OTHER INFORMATION: The peptide was designed and synthesized
                                                                                                                                                                                                   Score 60; DB 14; Length 15;
Pred. No. 0.0037;
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86.7%; Pred. No. 0.0037;
tive 1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                       US-10-056-583-63
Sequence 63, Application US/10056583
PUDIcation No. US20030064915A1
GENERAL INFORMATION:
APPLICANT: Presidents and Fellows of Harvard College
APPLICANT: Strominger, Jack L.
APPLICANT: Fridkis-Hareli, Masha
TITLE OF INVENTION: THERAPEUTIC PEPTIDES FOR DEMYELINATING
TITLE OF INVENTION: CONDITIONS
FILE REFERENCE: 24655-017
                                                                                                                                                                                                                                                  Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION NUMBER: US/10/056,583 CURRENT FILING DATE: 2002-01-24 PRIOR APPLICATION NUMBER: 60/263,569 PRIOR FILING DATE: 2001-01-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQ ID NOS: 99
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 63
LENGTH: 15
                                   LENGTH: 15
TYPE: PRT
ORGANISM: Artificial Sequence
PEATURE:
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ORGANISM: Artificial Sequence
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Best Local Similarity 86.7%;
Matches 13; Conservative
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ORGANISM: Artificial Sequence
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Matches 13; Conserv
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US-10-056-583-84
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          SEQ ID NO 55
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Sequence 51, Application US/10056583

Sublication No. US20030064915A1

SEGNERAL INFORMATION:

APPLICANT: Presidents and Fellows of Harvard College
APPLICANT: Strominger, Jack L.

APPLICANT: Fridkis-Hareli, Masha

TITLE OF INVENTION: THERAPEUTIC PEPTIDES FOR DEMYELINATING

TITLE OF INVENTION: CONDITIONS
FILE REFERENCE: 24655-017

CURRENT FALLING DATE: 2002-01-24

PRIOR APPLICATION NUMBER: 60/263,569

PRIOR FILING DATE: 2001-01-24

NUMBER OF SEQ ID NOS: 99

SOFTMARE: FastSEQ for Windows Version 4.0

SEQ ID NO 51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 55, Application US/10056583

Publication No. US20030064915A1

GENERAL INFORMATION:

APPLICANT: Presidents and Fellows of Harvard College
APPLICANT: Strominger, Jack L.

APPLICANT: Frickis-Harvali, Masha
TITLE OF INVENTION: THERAPEUTIC PEPTIDES FOR DEMYELINATING
TITLE OF INVENTION: CONDITIONS
FILE REFERENCE: 24655-017

CURRENT APPLICATION NUMBER: US/10/056,583

CURRENT FILING DATE: 2002-01-24

PRIOR APPLICATION NUMBER: 60/263,569

PRIOR PILING DATE: 2001-01-24

NUMBER OF SEQ ID NOS: 99

SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                  FEATURE:
; OTHER INFORMATION: The peptide was designed and synthesized. US-10-056-583-89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; OTHER INFORMATION: The peptide was designed and synthesized.
US-10-056-583-51
                                                                                                                                                                                                                                                                                                    Query Match

92.9%; Score 65; DB 14; Length 19;
Best Local Similarity 93.3%; Pred. No. 0.00074;
Matches 14; Conservative 0; Mismatches 1- Tradala
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93.3%; Pred. No. 0.00084;
tive 0; Mismatches 1
CURRENT FILING DATE: 2002-01-24
PRIOR APPLICATION NUMBER: 60/263,569.
PRIOR FILING DATE: 2001-01-24
NUMBER OF SEQ ID NOS: 99
SOFTWARE: PastSEQ for Windows Version 4.0
SEQ ID NO 89
                                                                                                                                                                     TYPE: PRT
ORGANISM: Artificial Sequence
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ORGANISM: Artificial Sequence
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Best Local Similarity
Matches 14; Conserva
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1 EAAKYEAYKAAAAA 15
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      13; Conservative
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US-10-056-583-61
           Matches
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GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Presidents and Fellows of Harvard College
APPLICANT: Presidents and Fellows of Harvard College
APPLICANT: Pridkis-Harell, Masha
ITILE OF INVENTION: CONDITIONS
FILE REPERENCE: 24655-017
CURRENT APPLICATION NUMBER: US/10/056,583
CURRENT APPLICATION NUMBER: 60/263,569
PRIOR FILING DATE: 2001-01-24
NUMBER OF SEQ ID NOS: 99
SOFTWARE: FREUENCE: 2001-01-24
NUMBER OF SEQ ID NOS: 99
SEQ ID NO 57
IENGTH: 15
                                                                                                                                                                                                                                                                                                 Sequence 86, Application US/10056583

Sequence 86, Application WO. 1022030064915A1

GENERAL INFORMATION:

APPLICANT: Presidents and Fellows of Harvard College
APPLICANT: Strominger, Jack L.

APPLICANT: Pridkis-Hareli, Masha

TITLE OF INVENTION: CONDITIONS

TITLE OF INVENTION: CONDITIONS

FILE REFERENCE: 24655-017

CURRENT APPLICATION NUMBER: US/10/056,583

CURRENT FILING DATE: 2002-01-24

PRIOR APPLICATION NUMBER: 60/263,569

SPRIOR FILING DATE: 2001-01-24

NUMBER OF SEQ ID NOS: 99

SOFURE OF SEQ ID NOS: 99

SEQ ID NO 86

LEASTER OF SEC ID NOS: 99
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; OTHER INFORMATION: The peptide was designed and synthesized.
US-10-056-583-57
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; OTHER INFORMATION: The peptide was designed and synthesized.
US-10-056-583-86
; OTHER INFORMATION: The peptide was designed and synthesized.
US-10-056-583-84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 60; DB 14; Length 15;
Pred. No. 0.0037;
0; Mismatches 2; Indels
                                                                         Score 60; DB 14; Length 15;
Pred. No. 0.0037;
                                                                         Query Match 85.7%; Score 60; DB Best Local Similarity 86.7%; Pred. No. 0.00 Matches 13; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; Sequence 57, Application US/10056583 ; Publication No. US20030064915A1
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ORGANISM: Artificial Sequence
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(1 Similarity 86.7%;
13; Conservative (
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Best Local Similarity
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US-10-056-583-57
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US-10-056-583-86
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Best Local S
Matches 13
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Sequence 95, Application US/10056583

Publication No. US20030064915A1

GENERAL INFORMATION:
APPLICANT: Presidents and Fellows of Harvard College
APPLICANT: Presidents and Fellows of Harvard College
APPLICANT: Fridkis-Hazeli, Masha
TITLE OF INVENTION: THERAPEUTIC PEPTIDES FOR DEMYELINATING
TITLE OF INVENTION: CONDITIONS
FILE REFERENCE: 24655-017
CURRENT APPLICATION NUMBER: US/10/056,583
CURRENT FILING DATE: 2002-01-24

RIOR APPLICATION NUMBER: 60/263,569

PRIOR FILING DATE: 2001-01-24

NUMBER OF SEQ ID NOS: 99

SOFTWARE: FastSEQ for Windows Version 4.0

LENGTH: 15
Sequence 61, Application US/10056583

Sequence 61, Application US/10056583

Publication No. US200064915A1

GRNERAL INFORMATION:
APPLICANT: Presidents and Fellows of Harvard College
APPLICANT: Strominger, Jack L.
APPLICANT: Fridkis-Hareli, Masha
TITLE OF INVENTION: THERAPEUTIC PEPTIDES FOR DEMYELINATING
TITLE OF INVENTION: CONDITIONS
FILE REPERENCE: 2465-017
CURRENT APPLICATION NUMBER: US/10/056,583
CURRENT FILING DATE: 2001-01-24
PRIOR FILING DATE: 2001-01-24
NUMBER: OF SEQ ID NOS: 99
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 61
LENGTH: 15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; OTHER INFORMATION: The peptide was designed and synthesized.
US-10-056-583-61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 84.3%; Score 59; DB 14; Length 15; Best Local Similarity 86.7%; Pred. No. 0.0054; Matches 13; Conservative 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM: Artificial Sequence
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1 EKAKFEAFKAAAAA 15
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ORGANISM: Artificial Sequence
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Best Local Similarity 80.03
Matches 12; Conservative
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RESULT 15
US-10-056-583-92

i Sequence 92, Application US/10056583

i Sequence 92, Application US/10056583

i Publication No. US20030064915A1

i GENERAL INFORMATION:

i APPLICANT: Presidents and Fellows of Harvard College

APPLICANT: Strominger, Jack L.

i APPLICANT: Fridkis-Hareli, Masha

TITLE OF INVENTION: THERAPEUTIC PEPTIDES FOR DEMYELINATING

TITLE OF INVENTION: CONDITIONS

FILE REPERBNCE: 24655-017

CURRENT APPLICATION NUMBER: US/10/056,583

CURRENT FILING DATE: 2002-01-24

NUMBER OF SEQ ID NOS: 99

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 92

LENGTH: 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: PRT ORGANISM: Artificial Sequence PATURE: PRATURE: PRATURE: PRATURE: COTHER INFORMATION: The peptide was designed and synthesized. US-10-056-583-92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 80.0%; Score 56; DB 14; Length 15; Best Local Similarity 86.7%; Pred. No. 0.016; Matches 13; Conservative 0; Mismatches 2; Indels
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1 EAAKYEAYKAAAAA 15 В

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Search completed: March 31, 2005, 02:48:48 Job time : 67.5323 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

March 31, 2005, 02:26:17 ; Search time 17.9032 Seconds (without alignments) 80.614 Million cell updates/sec Run on:

1 EAAKYEAYKAAAAA 15 US-10-056-583A-64 70 Perfect score: Sequence:

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

Searched:

283416 Total number of hits satisfying chosen parameters: 283416 segs, 96216763 residues

length: 0 length: 2000000000 Bed Bed Minimum DB 8 Maximum DB 8

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries Database :

PIR 79:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

		d			SUMMARIES	-
Result No.	Score	Query Match	Length	DB	ID	Description
	42	60.09	188	2	I50145	homeotic protein H
7	42	60.0		7	H86355	
e	42	60.0		~	A43562	homeotic protein H
4	42	0	527	7	E69351	_
2	41	58.6		7	E84764	hypothetical prote
9	41	58.6	1857	Н	S01787	
7	41	58.6	2129	~	T27431	hypothetical prote
80	40	57.1		N	C70521	1-acylglycerol-3-p
σ,	. 40	57.1		Н	GNVVSR	genome polyprotein
10	40	57.1	788	~	F97547	probable oxidoredu
11	40	57.1	788	7	AC2767	formate dehydrogen
12	40	57.1	Φ.	0	T13690	hypothetical prote
13	40	57.1	-	N	T18535	high molecular mas
14	39	55.7		~	G75512	conserved hypothet
15	39	55.7	170	~	E81312	probable lipoprote
16	39	55.7		N	T51971	proteasome endopep
17	39	55.7		N	839893	rnfC protein - Rho
18	39	55.7		~	D83640	hypothetical prote
19	39	55.7		-	QRMSE	
20		55.7		Н	QRRTE	estrogen receptor
21	39	55.7		~	T32594	hypothetical prote
22		55.7		~	H82965	DNA helicase II PA
23		54.3		7	F97521	VCO33 protein homo
24	38	54.3	108	7	AH2740	conserved hypothet
25	38	54.3	261	~	T51222	hypothetical prote
26	38	54.3	331	Н	DEECG3	glyceraldehyde-3-p
27	38	54.3	331	7	AG0711	glyceraldehyde 3-p
28	38	54.3	331	7	D85788	glyceraldehyde-3-p
29	38	54.3	331	~	H90939	glyceraldehyde-3-p

conserved hypothet Tola protein PA097	probable fatty-aci tetrahydrofolylpol folylpolyglutamate	hypothetical prote ATPase, AAA family H+-transporting to	efflux system prot related to protein probable fatty-aci	fatty acid synthas ribosomal protein transcription requ	T-cell receptor ga exoskeletal protei
C82156 E83525	T43037 B81936 C81170	E87463 D87408 S04675	E87470 T49355 T43409	T38781 B87702 G87606	S36290 S77930
0.0	000	0 0 0	000	0 0 0	0.0
346	377 424 424	428 433 478	478 521 1842	1842 165 176	185
54.3	54.3 54.3	54.3 54.3	54.3 54.3 54.3	54.3 52.9	52.9 52.9
38	8 8 8 7 7 7	888	3 8 8 8	38 37	37
30	33 34 34	35 36 37	33 38 4 0 9	4 4 4 4 2 2 3	4 4 5 4

ALIGNMENTS

homeotic protein Hox M -

C;Species: Gallus gallus (chicken)
C;Species: Gallus gallus (chicken)
C;Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 16-Aug-2004
C;Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 16-Aug-2004
C;Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 16-Aug-2004
R;Crompton, M.R.; MacGregor, A.D.; Goodwin, G.H.
Leukemia 5, 357-360, 1991
Leukemia 5, 357-360, 1991
A;Title: CDNA cloning of a homeobox-containing gene expressed in avian myeloblastic vin A;Reference number: 150145; MUID:91238215; PMID:1674560

A;Status: preliminary; translated from GB/EMBL/DDBJ A;Molecule type: mRNA A;Residues: 1-188 <CRO> A;Cross-references: UNIPROT:P23459; EMBL:X57158; NID:g62700; PIDN:CAA40445.1; PID:g62701

C;Genetics:

A,Gene: CHOX M C,Superfamily: homeobox homology C,Keywords: DNA binding; homeobox; nucleus; transcription regulation F;96-152/Domain: homeobox homology <HOX> Score 42; DB 2; Length 188; Pred. No. 9.8; 60.0%; 81.8%; Query Match

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Gaps

; 0

2; Indels

0; Mismatches

5 YEAYKAAAAA 15 ઠ

Local Similarity 81.8

Best Loc Matches

| ||||||| 10 YSKYKAAAAA 20 셤

probable 14-3-3 protein T16E15.8 - Arabidopsis thaliana (Fobbable 14-3-2) protein T16E15.8 - Arabidopsis thaliana (Fobbat: Cress)

Cipate: Oz-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004

Cipate: Oz-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004

Cipate: Oz-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004

R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K., Anture 408, 816-820, 2000

A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C. A.; Li, Y.; Liu, X.; Liu, X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali, Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.

A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, A;Refrence number: A66141; MUID:21016719; PMID:11130712

A;Accession: H86355

A;Status: preliminary A;Molecule type: DNA A;Residues: 1-254 <STO>

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Query Match
Best Local Similarity 60.0%;
Matches 9; Conservative 0
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Best Local Similarity 66.7%;
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 EAAKYEAYKAAAAA 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   hypothetical protein Y79H2A.3 -
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                                                                                                                                                                                                                                                                                                                                         A, Accession: E84764
A, Status: preliminary
A, Molecule type: DNA
A, Residues: 1-124 <STO>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         phosphoglycerate dehydrogenase (serA) homolog - Archaeoglobus fulgidus
C;Species: Archaeoglobus fulgidus
C;Species: Archaeoglobus fulgidus
C;Species: Archaeoglobus fulgidus
C;Species: Os-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 09-Jul-2004
C;Accession: E69551
R;Klenk, H.P.; Clayton, R.A.; Tomb, J.F.; White, O.; Nelson, K.E.; Ketchum, K.A.; Dodson, F.Fleischmann, R.D.; Quackenbush, J.; Lee, N.H.; Sutton, G.G.; Gill, S.; Kirkness, B.F.
Glodek, A.; Zhou, L.; Overbeek, R.; Gocayne, J.D.; Weidman, J.F.; McDonald, L.
Nature 390, 364-370, 1997
A;Authors: Utterback, T.; Cotton, M.D.; Spriggs, T.; Artiach, P.; Kaine, B.P.; Sykes, S.
Smith, H.O.; Woese, C.R.; Venter, J.C.
A;Title: The complete genome sequence of the hyperthermophilic, sulfate-reducing archaech
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Reaidues: 1-527 «KLE>
A;Cross-references: UNIPROT:029445; GB:AE001048; GB:AE000782; NID:92689371; PIDN:AAB9042
C;Superfamily: Bacillus phosphoglycerate dehydrogenase
A;Cross-references: UNIPROT:P48347; GB:AE005172; NID:99392684; PIDN:AAF87261.1; GSPDB:GN
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C;Species: Mus musculus (house mouse)
C;Date: 11-Dec-1992 #sequence_revision 11-Dec-1992 #text_change 09-Jul-2004
C;Accession: A43562 #sequence_revision 11-Dec-1992 #text_change 09-Jul-2004
C;Accession: A43562 #sequence_revision 11-Dec-1992 #text_change 09-Jul-2004
B;Izpisua-Belmonte, J.C.; Dolle, P.; Renucci, A.; Zappavigna, V.; Falkenstein, H.; Dubou Development 110, 733-745, 1990
A;Title: Primary structure and embryonic expression pattern of the mouse Hox-4.3 homeobd A;Title: Primary structure and embryonic expression pattern of the mouse Hox-4.3 homeobd A;Reference number: A43562
A;Status: preliminary; not compared with conceptual translation
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A;Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       N;Alternate names: homeotic protein Hox 4.3
C;Species: Mus musculus (house mouse)
C;Date: 11-Dec-1992 #sequence_revision 11-Dec-1992 #text_change 09-Jul-2004
                                                                                                                                                                                                        Gaps
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A,Residues: 1-289 - 1229-
A,Cross-references: UNIPROT:P23463
C,Superfamily: homeotic protein Hox A7; homeobox homology
C,Keywords: DNA binding; homeobox; nucleus; transcription regulation
F;196-252/Domain: homeobox homology <HOX>
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Pred. No. 15;
0; Mismatches 2; Indels
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Pred. No. 26;
0; Mismatches 5; Indels
                                                                                                                                             Score 42; DB 2; Length 254;
Pred. No. 13;
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                                                                                                                                                                                                     0; Mismatches
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                                                                                                                                             ch 60.0%;
1 Similarity 70.6%;
12; Conservative
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homeotic protein Hox D8 - mouse
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Best Local Similarity 81.0
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Best Local Similarity 66.73
Matches 10; Conservative
                                                          A;Map position: 1
C;Superfamily: 14-3-3 protein
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Best Local Similarity
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C;Accession: E84764
R;Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.; N.M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L.i. euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J. Nature 402, 761-768, 1999
A;Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A;Reference number: A84420; MUID:20083487; PMID:10617197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      R.Wiesner, P.; Beck, J.; Beck, K.F.; Ripka, S.; Mueller, G.; Luecke, S.; Schweizer, B. Bur. J. Blochem. 177, 69-79, 1988
A.Title: Isolation and sequence analysis of the fatty acid synthetase PAS2 gene from Peni. A;Reference number: S01787; MUID:89030697; PMID:3053172
A;Accession: S01787
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A,Cross-references: UNIPROT:082182; GB:AE002093; NID:93668094; PIDN:AAC61826.1; GSPDB:GN(
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A;Residues: 1-1857 <WIE>
A;Cross-references: UNIPROT:P15368; GB:M37461; NID:g169179; PIDN:AAA33695.1; PID:g169180
A;Note: the source is designated as Penicillium patulum
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;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
;Accession: S01787
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C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: T27431
R;Matthews, L.
hypothetical protein At2g35090 [imported] - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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Pred. No. 1.2e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 41; DB 2; Length 124; Pred. No. 9.7; 6; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         fatty-acid synthase (EC 2.3.1.85) - Penicillium griseofulvum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Caenorhabditis elegans
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A, Accession: T27431
A, Status: preliminary; translated from GB/EMBL/DDBJ
A, Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Status: not compared with conceptual translation; Molecule type: DNA
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C;Superfamily: yeast fatty-acid synthase
C;Keywords: acyltransferase; coenzyme A
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57.1%; Score 40;
61.5%; Pred. No.
                                                                     :|||| |: |||| ||
182 KAAKYAAFAARKKAAAVAA 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Gene: AGR C 2854
A;Map position: circular chromosome
C;Superfamily: formate dehydrogenase
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61.5%;
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343 AAEFEAYRAAVDA 355
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343 AAEFEAYRAAVDA 355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 61.57
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2 AAKYEAYKAAAA 14
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Best Local Similarity 61...
Best Coal Similarity 61...
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1-gaylglycerol-3-phosphate O-acyltransferase (EC 2.3.1.51) homolog - Mycobacterium tuber C; Species: Mycobacterium tuberculosis C; Species: Mycobacterium tuberculosis C; Species: Mycobacterium tuberculosis C; Species: Mycobacterium tuberculosis C; Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 16-Aug-2004 C; Accession: C70521 S. S. Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S. Rajanteam, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S. Nature 393, 537-544, 1998 A; Authors: Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G. A; Reference number: A70500; MUID:98295987; PMID:9634230 A; Reference number: A70500; MUID:98295987; PMID:9634230 A; Scatus: preliminary; nucleic acid sequence not shown; translation not shown A; Residues: 1-251 acOL; A; CCOL; A; Cross-references: UNIPROT:007808; GB:Z97188; GB:AL123456; NID:93261805; PIDN:CAB10008. A; Excession: C70521
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C;Species: tomato ringspot virus
C;Date: 30-Sep-1992 #sequence_revision 30-Sep-1992 #text_change 09-Jul-2004
C;Date: 30-Sep-1992 #sequence_revision 30-Sep-1992 #text_change 09-Jul-2004
C;Accession: A40787
N;Title: Comparison of the 5' and 3' termini of tomato ringspot virus RNA1 and RNA2: evi
A;Reference number: A40787; MUID:92024112; PMID:1926788
A;Accession: A40787
A;Residues: 1-354 <ROT>
A;Residues: 1-354 <ROT>
A;Residues: 1-354 <ROT>
C;Genetics:
A;Residues: 1-2129 <WIL>
A;Cross-references: UNIPROT:Q9UIR8; EMBL:AL110501; NID:e1542357; PIDN:CAB54509.1; CESP:Y
A;Experimental source: clone Y79H2A
C;Genetics:
A;Gene: CESP:Y79H2A.3
A;Gene: CESP:Y79H2A.3
A;Introns: 39/3; 75/1; 125/3; 212/3; 254/1; 330/3; 460/1; 486/3; 540/3; 580/3; 631/1; 67
i 1760/1; 1929/3; 2037/3; 2074/3
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C;Superfamily: commato ringspot virus genome polyprotein
C;Keywords: glycoprotein; polyprotein
F;270/Binding Bite: carbohydrate (Asn) (covalent) #status predicted
                                                                                                                                                                                                                         Length 2129;
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A;Gene: Rv381Sc
C;Superfamily: 1-acyl-sn-glycerol-3-phosphate acyltransferase
C;Keywords: acyltransferase; coenzyme A
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                                                                                                                                                                                                                      Score 41; DB 2; 1 Pred. No. 1.4e+02;
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Best Local Similarity 66.7%;
Matches 8; Conservative
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229 EAARMEADEAARAA 243
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144 EYAKYERYRSAA 155
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Matches 10; Conservative
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Matches 11; Conserva
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probable oxidoreductase (PA5181) [imported] - Agrobacterium tumefaciens (strain C58, Cer C; Species: Agrobacterium tumefaciens C; Species: Agrobacterium tumefaciens (2.5pecies: Agrobacterium tumefaciens (2.5pecies: Agrobacterium tumefaciens (2.5pecies: Agrobacterium tumefaciens (2.5paces) (2.5pac
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A;Molecule type: DNA
A;Residues: 1-788 <kUR>
A;Cross-references: UNIPROT:Q8UF51; GB:AE007869; PIDN:AAK87335.1; PID:g15156635; GSPDB:G
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A,Residues: 1-78 «KUR»
A,Gross-references: UNIRROT:Q8UF51; GB:AE008688; PIDN:AAL42553.1; PID:g17739976; GSPDB:C
A,Experimental source: strain C58 (Dupont)
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A;Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens CS8.
X;Reference number: AB2577; MUID:21608550; PMID:11743193
A;Accession: AC2767
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; Pred. No. 80;
3; Mismatches
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3; Mismatches
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Search completed: March 31, 2005, 02:42:27 Job time : 19.9032 secs
     Query Match 55.7%;
Best Local Similarity 50.0%;
Matches 7; Conservative
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Matches 7; Conservative
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C;Species: Drosophila melanogaster
C;Date: 13-Aug-1999 #sequence_revision 13-Aug-1999 #text_change 09-Jul-2004
C;Date: 13-Aug-1999 #sequence_revision 13-Aug-1999 #text_change 09-Jul-2004
C;Date: 13-Aug-1999 #sequence_revision 13-Aug-1999 #text_change 09-Jul-2004
R;Murphy, L: Harris, D.; Barrell, B.
submitted to the EMBL Data Library, November 1998
A;Description: Sequencing the distal X chromosome of Drosophila melanogaster.
A;Description: Sequencing the distal X chromosome of Drosophila melanogaster.
A;Accession: T13590
A;Accession: T13590
A;Accession: T13590
A;Accession: T1806 cMUR>
A;Accession: T1806 cMUR>
A;Residues: 1-806 cMUR>
C;Genetics:
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C;Species: Gallus gallus (chicken)
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: T18535
C;Accession: T18535
J; Call Sci. 110, 3031-3041, 1997
J; Call Sci. 110, 3031-3041, 1997
A;Fitle: A muclear matrix-associated high molecular mass nuclear antigen, HMNA, of chick A;Accession: T18535
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A,Status: preliminary; translated from GB/EMBL/DDBJ
A,Modecule type: mRNA
A,Residues: 1-1151 cSHI>
A,Cross-references: UNIPROT:057580; EMBL:D88440; NID:d1177138; PID:d1025045; PIDN:BAA241
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C;Species: Deinococcus radiodurans
C;Species: Deinococcus radiodurans
C;Species: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
C;Acces: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
C;Acces: 03-Dec-1999 #sequence 075512 Hickey, E.K.; Peterson, J.D.; Dodson, R.J.;
R;White, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, R.J.;
M.; Shen, M.; Vamathevan, J.J.; Lam, P.; McDonald, L.; Utterback, T.; Zalewski, C.; Ma Science 26, 1571-1577, 1999
A;Fitle: Genome sequence of the radioresistant bacterium Deinococcus radiodurans R1.
A;Reference number: A75250; MUID: 20036896; PMID: 10567266
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A,Residues: 1-101 <WHI>
A,Cross-references: UNIPROT:09RX23; GB:AE001908; GB:AE000513; NID:g6458174; PIDN:AAF1006
Experimental source: strain R1
C,Genetics:
A,Gene: DR0492
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high molecular mass nuclear antigen - chicken (fragment)
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Pred. No.
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A;Introns: 37/3; 448/3; 611/2; 690/3
A;Note: EG:EG0003.2
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69.2%;
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Best Local Similarity
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C,Accession: E81312
R;Parkhill, J.; Wren, B.W.; Mungall, K.; Ketley, J.M.; Churcher, C.; Basham, D.; Chilling C.W.; Quall, M.; Rajandream, M.A.; Rutherford, K.M.; VanVliet, A.; Whitehead, S.; Barrell Nature 403, 665-668, 2000
A;Title: The genome sequence of the food-borne pathogen Campylobacter jejuni reveals hype A;Reference number: A81250; MUID:20150912; PMID:10688204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A,Cross-references: UNIPROT:09PNK4; GB:AL139077; GB:AL111168; NID:g6968444; PIDN:CAB73344:
A,Experimental source: serotype O2, strain NCTC 11168
                                                                                                                                                                                                                                                                                                                             probable lipoprotein Cj1090c [imported] - Campylobacter jejuni (strain NCTC 11168)
C;Species: Campylobacter jejuni
C;Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 09-Jul-2004
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Length 101;
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28;
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                                                             Indels
Score 39; DB 2;
Pred. No. 17;
4; Mismatches
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Galagan J.B., Calvo S.E., Borkovich K.A., Selker E.U., Read N.D., Jaffe D., FitzHugh W., Ma L.-J., Smirnov S., Purcell S., Rehman B., Bitins T., Engels R., Wang S., Nielsen C.B., Butler J., Endrizzi M., A Litsins T., Engels R., Wang S., Nielsen C.B., Butler J., Endrizzi M., Selitrennikoff C.P., Kinsey J.A., Braun E.L., Zelter A., Schulte U., Selitrennikoff C.P., Kinsey J.A., Braun E.L., Zelter A., Schulte U., Roy d., Jedg G., Mewes W., Staben C., Marcotte E., Greenberg D., Roy A., Foley K., Naylor J., Mauceli E., Bielke C., Rudd S., Frishman D., Krystofova S., Rasmussen C., Metzenberg R.L., Perkins D.D., Kroken S., Arstofova S., Rasmussen C., Metzenberg R.L., Perkins D.D., Kroken S., DeSouza C.C., Glass L., Orbach M.J., Berglund J., Voelker R., Yarden O., Plamann M., Seiler S., Dunlap J., Rafford A., Aramayo R., Natvig D.O., Alex L.A., Mannhaupt G., Ebbole D.J., Freitag M., Paulsen I., Sachs M.S., Lander E.S., Nusbaum C., Birren B., The Genome Sequence of the Filamentous Fungus Neurospora crassa.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Nature 0:0-0(2003).
-1- CAUTION: The sequence shown here is derived from an EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      847 AA; 94963 MW; CDAF7CSDSEFD910A CRC64;
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Best Local Similarity 66.7%; Pred. No. 56;
Matches 10; Conservative 1; Mismatches
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EMBL, AABXO1000143; EAA34000.1; -.
InterPro; IPR004648; Oligpept_transpt.
InterPro; IPR004613; Tetrpept_transpt.
Pfam; PF03169; OPT; 1.
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TIGRFAMS; TIGR00728; OPT_Sfam; 1.
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                                                                                                                                    March 31, 2005, 02:18:02; Search time 80.5645 Seconds (without alignments) 95.342 Million cell updates/sec
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                                                                                                                                           1612378 segs, 512079187 residues
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HXD8 MOUSE
Q8IXZ1
HXD8 HUMAN
Q6ATQ1
Q8W0D1
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Q87S\frac{7}{7}7
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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1: uniprot_sprot:*
2: uniprot_trembl:*
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seq length: 200000000
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Gaps

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Length 847; 4; Indels

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Bukaryota, Fungi, Ascomycota, Pezizomycotina, Sordariomycetes,
Sordariomycetidae, Sordariales, Sordariaceae, Neurospora.
06i5h3
02945
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0964jw6
0084jw6
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Last annotation update)
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        SERA ARCFU
Q64JV6
                           Q9NDJ0
Q64JW6
Q7S637
CU02 BLACR
O82182
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Q6YWS1
Q8IRS8
Q6AV91
Q6QUT5
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 5527
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SEQUENCE FROM N.A.
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"Plasmodium vivax merozoite surface protein PvMSP-3beta is radically polymorphic through mutation and large insertions and deletions."; Infect. Genet. Evol. 4:309-319 (2004).
EMBL; AY454085; AAS10471.1; -.
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EMBL; AY454094; AAS10480.1; -.
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Rayner J.C., Huber C.S., Feldman D., Ingravallo P., Galinski M.R.,
Barnwell J.W.;
                                                                                                                                                                                                             PubMed=15374528;
Rayner J.C., Huber C.S., Feldman D., Ingravallo P., Galinski M.R.,
Barnwell J.W.;
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                                                                                  Plasmodium vivax.
Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
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608 AA; 65845 MW; A07CDB0563F4FE03 CRC64;
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25-OCT-2004 (TrEMBLrel. 28, Created)
25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
25-OCT-2004 (TrEMBLrel. 28, Created)
25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
Merozoite surface protein 3b (Fragment).
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25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
Merozoite surface protein 3b (Fragment).
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0; Mismatches
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Les 11, Conservative
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Infect. Genet. Evol. 4:309-319(2004).
EMBL; AY454088; AAS10474.1; -.
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EMBL; AX454087; AAS10473.1; -.
                                                                                                                                                                                                                                                    STRAIN=Br781B;
PubMed=15374528;
Rayner J.C., Huber C.S., Feldman D., Ingravallo P., Galinski M.R.,
Barnwell J.W.;
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PubMed=15374528;
Rayner J.C., Huber C.S., Feldman D., Ingravallo P., Galinski M.R.,
Barnwell J.W.;
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25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
Merozoite surface protein 3b (Fragment).
Plasmodium vivax.
Eukaryota, Alveolata, Apicomplexa, Haemosporida, Plasmodium.
NCBL TaxID=5855,
                                                                                                                                                  Plasmodium vivax.
Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
NCBI_TaxID=5855;
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603 603
603 AA, 65111 MW, 9FB464A42ED295C4 CRC64;
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                 Q64JV8 PRELIMINARY, PRT; 603 AA. Q64JV8; C5-CCT-2004 (TrEMBLrel. 28, Created) 25-CCT-2004 (TrEMBLrel. 28, Last sequence update) 25-CCT-2004 (TrEMBLrel. 28, Last annotation update) Merozoite surface protein 3b (Fragment).
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"Plasmodium vivax merozoite surface protein PvMSP-3beta is radically polymorphic through mutation and large insertions and deletions."; Infect. Genet. Evol. 4:309-319(2004).
EMBL; AY454089; AAS10475.1; -.
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EMBL; AY454092; AAS10478.1; -.
                                                                               PubMed=15374528;
Rayner J.C., Huber C.S., Feldman D., Ingravallo P., Galinski M.R.,
Barnwell J.W.;
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Rayner J.C., Huber C.S., Feldman D., Ingravallo P., Galinski M.R.,
Barnwell J.W.;
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NCBL_TaxID=5855;
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NCBI_TaxID=5855;
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810 Aa; 86539 MW; 14B1E39FAE44F74A CRC64;
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25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
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EMBL; AY454093; AAS10479.1;
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Rayner J.C., Huber C.S., Feldman D., Ingravallo P., Galinski M.R.,
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NCBI_TaxID=5855;
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25-OCT-2004 (TrEMBLrel. 28, Created)
25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
Merozoite surface protein 3b (Fragment).
Plasmodium vivax.
Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
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727 AA; 78556 MW; B3A309A6874F5B0D CRC64;
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Rayner J.C., Huber C.S., Feldman D., Ingravallo P., Galinski M.R.,
Barnwell J.W.;
Barnwell J.W.;
"Plasmodium vivax merozoite surface protein PvMSP-3beta is radically
polymorphic through mutation and large insertions and deletions.";
Infect. Genet. Evol. 4:309-319(2004).
EMBL; AY454081; AAS10467.1; --
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Rayner J.C., Huber C.S., Feldman D., Ingravallo P., Galinski M.R.,
Barnwell J.W.;
"Plasmodium vivax merozoite surface protein PvMSP-3beta is radically
                                                                                                                                                                                      "Plaamodium vivax merozoite surface protein PvMSP-3beta is radically polymorphic through mutation and large insertions and deletions."; Infect. Genet. Evol. 4:309-319(2004).

EMBL; AY454083; AAS10469.1; -.
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                                                                                   Rayner J.C., Huber C.S., Feldman D., Ingravallo P., Galinski M.R., Barnwell J.W.;
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NCBL_TaxID=5855;
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Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
NCBI _TaxID=5855;
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Pred. No. 86;
0; Mismatches 3; Indels
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Pred. No. 80;
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826 AA; 89752 MW; 699B1F21F5B747B6 CRC64;
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25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
Merozoite surface protein 3b (Fragment).
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78.6%;
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                                                           PubMed=15374528;
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AC 064JWW
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DT 25-0C
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OS BURAZ
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"Plasmodium vivax merozoite surface protein PvMSP-3beta is radically polymorphic through mutation and large insertions and deletions."; Infect. Genet. Evol. 4:309-319(2004).

EMBL; AX454095; AAS10481.1; -.
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Barnwell J.W.;
polymorphic through mutation and large insertions and deletions."; Infect. Genet. Evol. 4:309-319(2004). EMBL; AY454082; AAS10468.1; -.
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Bukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea; Aedes.
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                                                                                                                                                                                                                        Score 45; DB 2; Length 900;
Pred. No. 86;
0; Mismatches 3; Indels
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Submitted (MAY-2004) to the EMBL/GenBank/DDBJ databases.

Submitted (MAY-2004) to the EMBL/GenBank/DDBJ databases.

EMBL, AY663380; AAT69676.1; -.

GO, GO:00165020; C:membrane; IEA.

GO, GO:0005261; F:cation channel activity; IEA.

GO; GO:0006812; P:cation transport; IEA.

InterPro; IPR005821; Ion trans.

InterPro; IPR005820; M+channel_nlg.
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25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
Voltage dependent para-like sodium channel (Fragment).
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927 AA; 99734 MW; B5DCBD6130A7F4E1 CRC64;
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900 AA; 97231 MW; DC84487C0D34BF7B CRC64;
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25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
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78.6%;
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25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
Voltage-dependent para-like sodium channel (Fragment).
Aedes albopictus (Forest day mosquito).
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea; Aedes.
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Bubmitted (MAY-2004) to the EMBL/GenBank/DDBJ databases.

R EMBL, AY663381; AAT6697.1.;

R GO; GO:0016200; C:membrane; IEA.

R GO; GO:0016261; F:cation channel activity; IEA.

R GO; GO:0016812; F:cation transport; IEA.

R GO; GO:0016812; P:cation transport; IEA.

R InterPro; IPR005820; M+channel_nlg.

R InterPro; IPR005820; M+channel_nlg.

R InterPro; IPR005820; M+channel_nlg.

R InterPro; IPR005820; M+channel]. Transmembrane; Transport.

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NON TER 509 509

SEQÜENCE 509 AA; 56992 MW; 2D3DCB47D423D5C0 CRC64;
                                                                                                                                                62.9%; Score 44; DB 2; Length 501; 73.3%; Pred. No. 73; ive 1; Mismatches 3; Indels
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Pfam; PP00520; Ion_trans; 2.
Ion transport; Ionic channel; Transmembrane; Transport.
NON_TER 1 51
NON_TER 501 S01
SEQÜENCE 501 AA; 56497 MW; B66CD123B5EC5FDD CRC64;
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76 KAAKLEAQAAAAAA 90
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Best Local Similarity 73.39
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Search completed: March 31, 2005, 02:41:07 Job time : 82.5645 secs

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2105692 Total number of hits satisfying chosen parameters: 2105692 seqs, 386760381 residues BLOSUM62 Gapop 10.0 , Gapext 0.5 1 APEKAKYEAYKAAAAA 17 US-10-056-583A-88 82 Perfect score: Scoring table: Sequence: Searched:

seq length: 0 seq length: 2000000000 08 08 Minimum Maximum

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries geneseqp2003as:* geneseqp2003bs:* A_Geneseq_16Dec04:* geneseqp1990s:* geneseqp2000s:* geneseqp2001s:* geneseqp2002s:* geneseqp2004s:* geneseqp1980s:* Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Description	2294 HLA-DR2 m	295 HLA-DR2 m	303 HLA-DR2 m	н	298 HLA-DR2 m	296 HLA-DR2 m	302 HLA-DR2 m	270 HLA-DR2 m	301 HLA-DR2 m	291 HLA-DR2 m	263 HLA-DR2 m	272 HLA-DR2 m	259 HLA-DR2 m	257 HLA-DR2 m	297 HLA-DR2 m	253 HLA-DR2 m	251 HLA-DR2 m	239 HLA-DR2 m	290 HLA-DR2 m	261 HLA-DR2 m	244 HLA-DR2 m	292 HLA-DR2 m	269 HLA-DR2 m	262 HLA-DR2 m	264 HLA-DR2 m
	Desci	Abp52	Abp5229	Abp523	Abp5227	Abp522	Abp5229(Abp52302	Abp5227	Abp52301	Abp5229	Abp52263	Abp52	. Abp52259	Abp52	Abp52	Abp52253	Abp52251	Abp52	Abp5229(Abp52261	Abp52244	Abp52	Abp52269	Abp52	Abp523
SOMERALES	ID	ABP52294	ABP52295	ABP52303	ABP52271	ABP52298	ABP52296	ABP52302	ABP52270	ABP52301	ABP52291	ABP52263	ABP52272	ABP52259	ABP52257	ABP52297	ABP52253	ABP52251	ABP52239	ABP52290	ABP52261	ABP52244	ABP52292	ABP52269	ABP52262	ABP52264
	Match Length DB	17 5										15 5											_			
* 5	Match	100.0	100.0	89.0	96.6	9.98	96.6	84.1	79.3	76.8	74.4	74.4	73.2	72.0	72.0	69.5	68.3	68.3	68.3	67.1	67.1	67.1	67.1	67.1	67.1	62.9
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Abp52267 Abp52236	Abp52299	Abp52265	Abp52254	Abp52255	Abp52240	Abp52241	Abp52304	Abp52248	Abp52249	Abp52232	Abp52268	Abp52231	Ada55549	Adj70708	Abp52235	Abp52250	Abp52277	Abp52238
ABP52267 ABP52236	ABP52299	ABP52265	ABP52254	ABP52255	ABP52240	ABP52241	ABP52304	ABP52248	ABP52249	ABP52232	ABP52268	ABP52231	ADA55549	ADJ70708	ABP52235	ABP52250	ABP52277	ABP52238
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26	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

Human leukocyte antigen; HLA; major histocompatibility complex; MHC; HLA-DR2; MHC class II DR-2 molecule; demyelinating; multiple sclerosis; immune response; antiinflammatory; neuroprotective; proliferation; MHC class II protein inhibitor; demyelinating disease; inhibition; post-viral encephalomyelitis; post-vaccine demyelinating condition; anti-tumour necrosis factor agent. HLA-DR2 molecule binding peptide SEQ ID NO:88. ABP52294 standard; peptide; 17 AA. (first entry) 16-OCT-2002 ABP52294;

WO200259143-A2. Homo sapiens Synthetic.

24-JAN-2002; 2002WO-US002071. 24-JAN-2001; 2001US-0263569P.

01-AUG-2002.

Strominger JL, Fridkis-Hareli M;

(HARD) HARVARD COLLEGE.

WPI; 2002-608439/65.

ø a major treating New compositions comprising synthetic peptides in complex with histocompatibility complex class II HLADR2 protein, useful for demyelinating disease, e.g. multiple sclerosis, or post-viral encephalomyelitis.

Claim 28; Page 39; 54pp; English.

The present invention describes compositions (I) comprising a peptide with an amino acid sequence with tyrosine (Y), lysine (K), and/or valine residues. The complex of the peptide with a major histocompatibility complex (MHC) class II HLA-DR2 protein is involved in modulating an immune response. (I) has antiniflammatory and neuroprotective activities, and can be used as a MHC class II protein inhibitor. The compositions comprising the peptides are useful for treating demyelinating diseases

Gaps

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Indels

0; Mismatches

1 APEKAKYEAYKAAAAA 17

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17

APEKAKYEAYKAAAAA

Score 82; DB 5; Length 19; Pred. No. 1.8e-06;

100.08;

100.0%;

17, Conservative

Local Similarity

Query Match Best Loc Matches

Sequence 19 AA;

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such as multiple sclerosis, post-viral encephalomyelitis, a post-vaccine demyelinating condition, and a side effect of administering an antitumour necrosis factor agents. The peptide further inhibits proliferation of autoantigen-specific HLA-DR2-restricted T call clones. ABP52207 to ABP52305 represent peptides used in the exemplification of the present
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Human leukocyte antigen; HLA; major histocompatibility complex; MHC; HLA-DR2; MHC class II DR-2 molecule; demyelinating; multiple sclerosis; immune response; antiinflammatory; neuroprotective; proliferation; MHC class II protein inhibitor; demyelinating disease; inhibition; post-viral encephalomyelitis; post-vaccine demyelinating condition;

anti-tumour necrosis factor agent.

sapiens.

Ношо

Synthetic.

24-JAN-2002; 2002WO-US002071.

WO200259143-A2.

01-AUG-2002.

24-JAN-2001; 2001US-0263569P

HLA-DR2 molecule binding peptide SEQ ID NO:97.

(first entry)

16-OCT-2002

ABP52303;

ABP52303 standard; peptide; 17 AA.

RESULT 3 ABP52303

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The present invention describes compositions (I) comprising a peptide with an amino acid sequence with tyrosine (Y), lysine (R), and/or value residues. The complex of the peptide with a major histocompatibility complex (MHC) class II HIA-DR2 protein is involved in modulating an immune response. (I) has antiinflammatory and neuroprotective activities, and can be used as MHC class II protein inhibitor. The compositions comprising the peptides are useful for treating demyelinating diseases such as multiple sclerosis, post-viral encephalomyelitis, a post-vaccine demyelinating condition, and a side effect of administering an antitumour necrosis factor agents. The peptide further inhibits proliferation of autoantigen-specific HIA-DR2-restricted T cell clones. ABB52207 to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New compositions comprising synthetic peptides in complex with a major histocompatibility complex class II HLADR2 protein, useful for treating demyelinating disease, e.g. multiple sclerosis, or post-viral encephalomyelitis.
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Best Local Similarity 88.2
Matches 15; Conservative
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The present invention describes compositions (1) comprising a peptide with an amino acid sequence with tyrosine (Y), lysine (K), and/or valine residues. The complex of the peptide with a major histocompatibility complex (MHC) class II HLA-DR2 protein is involved in modulating an immune response. (I) has antiinflammatory and neuroprotective activities, and can be used as a MHC class II protein inhibitor. The compositions comprising the peptides are useful for treating demyelinating diseases such as multiple sclerosis, post-viral encephalomyelitis, a post-vaccine demyelinating condition, and a side effect of administering an anti-tumour necrosis factor agents. The peptide further inhibits proliferation of autoantigen-specific HLA-DR2-restricted T cell clones. ABB52207 to

Invention

ABP52298;

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The present invention describes compositions (I) comprising a peptide with an amino acid sequence with tyrosine (Y), lysine (K), and/or valine residues. The complex of the peptide with a major histocompatibility complex (MHC) class II HLA-DE2 protein is involved in modulating an immune response. (I) has antiinflammatory and neuroprotective activities, and can be used as a MHC class II protein inhibitor. The compositions comprising the peptides are useful for treating demyelinating diseases such as multiple sclerosis, post-viral encephalomyalitis, a post-vaccine demyelinating condition, and a side effect of administering an antituour necrosis factor agents. The peptide further inhibits proliferation of autoantigen-specific HLA-DE2-restricted T cell clones. ABBF52307 to ABBF53305 represent peptides used in the exemplification of the present
                                                                                                                                                                                                                                             Human leukocyte antigen; HLA; major histocompatibility complex; MHC; HLA-DR2; MHC class II DR-2 molecule; demyelinating; multiple sclerosis; immune response; antiinflammatory; neuroprotective; proliferation; MHC class II protein inhibitor; demyelinating disease; inhibition; post-viral encephalowyelitis; post-vaccine demyelinating condition;
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Pred. No. 8.8e-05;
0; Mismatches 0; Indels
                                                                                                                                                                                                            HLA-DR2 molecule binding peptide SEQ ID NO:65.
                                                                                                      ABP52271 standard; peptide; 15 AA.
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24-JAN-2002; 2002WO-US002071.
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treating
                                                                                                         Human leukocyte antigen; HLA; major histocompatibility complex; MHC; HLA-DR2; MHC class II DR-2 molecule; demyelinating; multiple sclerosis; immune response; antiinflammatory; neuroprotective; proliferation; MHC class II protein inhibitor; demyelinating disease; inhibition; post-viral encephalomyelitis; post-vaccine demyelinating condition; anti-tumour necrosis factor agent.
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Pred. No. 8.8e-05;
0; Mismatches 0;
                                                                             HLA-DR2 molecule binding peptide SEQ ID NO:92.
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                                              16-OCT-2002 (first entry)
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Matches 15; Conservative
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Gaps ö

ABP52298 standard; peptide; 15 AA.

RESULT 5 ABP52298 ID ABP5

EKAKYEAYKAAAAA 15

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sapiens.

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New compositions comprising synthetic peptides in complex with a major histocompatibility complex class II HLADR2 protein, useful for treating demyelinating disease, e.g. multiple sclerosis, or post-viral
Human leukocyte antigen; HLA; major histocompatibility complex; MHC; HLA-DR2; MHC class II DR-2 molecule; demyelinating; multiple sclerosis; immune response; antiinflammatory; neuroprotective; proliferation; MHC class II protein inhibitor; demyelinating disease; inhibitor; post-viral encephalomyelitis; post-vaccine demyelinating condition;
                                                             anti-tumour necrosis factor agent
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                                                                                    Homo sapiens.
Synthetic.
                                                                                                                                                 01-AUG-2002.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      invention
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0 The present invention describes compositions (I) comprising a peptide with an amino acid sequence with tyrosine (Y), lysine (K), and/or valine residues. The complex of the peptide with a major histocompatibility complex (MHC) class II HLA-DE2 protein is involved in modulating an immune response. (I) has antiinflammatory and neuroprotective activities, and can be used as a MHC class II protein inhibitor. The compositions comprising the peptides are useful for treating demy-linating diseases such as multiple sclerosis, post-viral encephalomyelitis, a post-vaccine demyelinating condition, and a side effect of administering an antitumour necrosis factor agents. The peptide further inhibits proliferation of autoantigen-specific HLA-DE2-restricted T cell clones. ABBPS207 to Gaps

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1 APEKAKFEAFKAAAAPA 17

ö 86.6%; Score 71; DB 5; Length 17; 100.0%; Pred. No. 0.0001; ive 0; Mismatches 0; Indels 15; Conservative Query Match Best Local Similarity ო Matches ò

EKAKYEAYKAAAAA 17 EKAKYEAYKAAAAA 15

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ABP52302 standard; peptide; 17 ABP52302; RESULT 7
ABP52302
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XX
DT 16-0
XX
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DD HLAXX
XW HUMA
XW HUMA
XW HUMA
XW HUMA
XW MHC
XW M

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16-OCT-2002 (first entry)

HLA-DR2 molecule binding peptide SEQ ID NO:96.

Human leukocyte antigen, HLA, major histocompatibility complex, MHC, HLA-DR2; MHC class II DR-2 molecule, demyelinating, multiple sclerosis, immune response, antiinflammatory, neuroprotective, proliferation, MHC class II protein inhibitor; demyelinating disease; inhibition; post-viral encephalomyelitis; post-vaccine demyelinating condition; anti-tumour necrosis factor agent.

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The present invention describes compositions (I) comprising a peptide with an amino acid sequence with tyrosine (Y), lyaine (K), and/or valine residues. The complex of the peptide with a major histocompatibility complex (MHC) class II HIA-DR2 protein is involved in modulating an immune response. (I) has antiinflammatory and neuroprotective activities, and can be used as a MHC class II protein inhibitor. The compositions comprising the peptides are useful for treating demylains diseases such as multiple sclerosis, post-viral encephalomyelitis, a post-vaccine demyelinating condition, and a side effect of administering an antitumour necrosis factor agents. The peptide further inhibits proliferation of autcoantigen-specific HIA-DR2-restricted T cell clones. ABP52207 to
                                                                                                                                                                                                                                                                                                                  New compositions comprising synthetic peptides in complex with a major histocompatibility complex class II HLADR2 protein, useful for treating demyelinating disease, e.g. multiple sclerosis, or post-viral
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        84.1%; Score 69; DB 5; Length 17; 82.4%; Pred. No. 0.00021; ive 2; Mismatches 1; Indels
                                                                                                                                                                                                                                            Strominger JL, Fridkis-Hareli M;
                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 28; Page 39; 54pp; English.
                                                                                                                             24-JAN-2002; 2002WO-US002071
                                                                                                                                                                 24-JAN-2001; 2001US-0263569P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 84.1
Best Local Similarity 82.4
Matches 14; Conservative
                                                                                                                                                                                                      (HARD ) HARVARD COLLEGE
                                                                                                                                                                                                                                                                               WPI; 2002-608439/65
                                                                                                                                                                                                                                                                                                                                                                              encephalomyelitis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 17 AA;
                                                     WO200259143-A2
                                                                                        01-AUG-2002
Homo sapie
Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               nvention
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HLA-DR2 molecule binding peptide SEQ ID NO:64. 16-OCT-2002 (first entry) ABP52270;

ABP52270 standard; peptide; 15 AA.

RESULT 8

Human leukocyte antigen; HLA; major histocompatibility complex; MHC; HLA-DR2; MHC class II DR-2 molecule; demyelinating; multiple sclerosis; immune response; antiinflammacory; neuroprotective; proliferation; MHC class II protein inhibitor; demyelinating disease; inhibition; post-viral encephalomyelitis; post-vaccine demyelinating condition; anti-tumour necrosis factor agent.

sapiens. Synthetic

WO200259143-A2

01-AUG-2002.

4

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The present invention describes compositions (I) comprising a peptide with an amino acid sequence with tyrosine (Y), lysine (K), and/or valine residues. The complex of the peptide with a major histocompatibility complex (MHC) class II HLA-DR2 protein is involved in modulating an immune response. (I) has antiinflammatory and neuroprotective activities, and can be used as a MHC class II protein inhibitor. The compositions comprising the peptides are useful for treating demyelinating diseases such as multiple sclerosis, post-viral encephalomyelitis, a post-vaccine demyelinating condition, and a side effect of administering an antitumour necrosis factor agents. The peptide further inhibits proliferation of autoantigen-specific HLA-DR2-restricted T cell clones. ABP52307 to ABP52305 represent peptides used in the exemplification of the present
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                                                                                                          New compositions comprising synthetic peptides in complex with a major histocompatibility complex class II HLADR2 protein, useful for treating a demyelinating disease, e.g. multiple sclerosis, or post-viral encephalomyelitis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 63; DB 5; Length 15;
Pred. No. 0.0018;
; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HLA-DR2 molecule binding peptide SEQ ID NO:85.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ABP52291 standard; peptide; 15 AA.
                                                                                                                                                                                                                                                                            Claim 28; Page 39; 54pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Strominger JL, Fridkis-Hareli M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2;
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86.7%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 EKAKFEAFKAAAAA 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 86.7
Matches 13; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             16-OCT-2002 (first entry)
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                                          WPI; 2002-608439/65.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 15 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WO200259143-A2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   invention
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       with an amino acid sequence with typosine (N; lysine (K), and/or valine residues. The complex of the peptide with a major histocompatibility complex (Rtc) class II HLA-DR2 protein is involved in modulating an immune response. (I) has antiinflammatory and neuroprotective activities, and can be used as a MHC class II protein inhibitor. The compositions comprising the peptides are useful for treating demyslinating diseases such as multiple sclerosis, post-viral encephalomyelitis, a post-vaccine demyelinating condition, and a side effect of administering an anti-umour necrosis factor agents. The peptide further inhibits proliferation of autoantigen-specific HLA-DR2-restricted T cell clones, ABP52207 to
                                                                                                                                                                                                                                                                                                                                            New compositions comprising synthetic peptides in complex with a major histocompatibility complex class II HLADR2 protein, useful for treating demyelinating disease, e.g. multiple sclerosis, or post-viral
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human leukocyte antigen; HLA; major histocompatibility complex; MHC; HLA-DR2; MHC class II DR-2 molecule; demyelinating; multiple sclerosis; immune response; antinflammatory; neuroprotective; proliferation; MHC class II protein inhibitor; demyelinating disease; inhibition; post-viral encephalomyelitis; post-vaccine demyelinating condition; anti-tumour necrosis factor agent.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The present invention describes compositions (I) comprising a peptide
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Pred. No. 0.00085;
0; Mismatches 1; Indels
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                                                                                                                                                                                                         Strominger JL, Fridkis-Hareli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ABP52301 standard; peptide; 15
24-JAN-2002; 2002WO-US002071.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 79.3%;
                                                                      24-JAN-2001; 2001US-0263569P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Beet Local Similarity > ...
Local 14; Conservative
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                                                                                                                                      (HARD ) HARVARD COLLEGE
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                                                                                                                                                                                                                                                                         WPI; 2002-608439/65.
                                                                                                                                                                                                                                                                                                                                                                                                                                               encephalomyelitis.
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RESULT 9

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with an amino acid sequence with tyrosine (X), lysine (X), and/or value residues. The complex of the peptide with a major histocompatibility complex. The complex of the peptide with a major histocompatibility immune response. (I) has antiinflammatcry and neuroprotective activities and can be used as a MHC class II protein inhibitor. The compositions comprising the peptides are useful for treating demyelinating diseases such as multiple sclerosis, post-viral encephalomyelitis, a post-vacine demyelinating condition, and a side effect of administering an antitumour necrosis factor agents. The peptide further inhibits proliferation of autoantigen-specific HLA-DRZ-restricted T cell clones. ABP52307 to
                                                                                                                                                                                                                                                                                                                                                                                                               Score 61; DB 5; Length 15;
Pred. No. 0.0039;
0; Mismatches 2; Indels
                                                                    compositions (I)
                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Mismatches
                      Claim 28; Page 39; 54pp; English
                                                               present invention describes
                                                                                                                                                                                                                                                                                                                                                                                                                      74.48;
                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity 86.7
Matches 13; Conservative
                                                                                                                                                                                                                                                                                                                                                                          Sequence 15 AA;
                                                                                                                                                                                                                                                                                                                                  invention
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ABP52263 standard; peptide; 15 AA. RESULT 11

(first entry) 16-OCT-2002 ABP52263;

HLA-DR2 molecule binding peptide SEQ ID NO:57.

Human leukocyte antigen, HLA; major histocompatibility complex; MHC; HLA-DR2; MHC class II DR-2 molecule; demyelinating; multiple sclerosis; immune response; antiinflammatory; neuroprotective; proliferation; MHC class II protein inhibitor; demyelinating disease; inhibition; post-viral encephalomyelitis; post-vaccine demyelinating condition; anti-tumour necrosis factor agent.

sapiens Homo

Synthetic

WO200259143-A2.

01-AUG-2002.

24-JAN-2001; 2001US-0263569P. 24-JAN-2002; 2002WO-US002071.

(HARD) HARVARD COLLEGE

Ξ Fridkis-Hareli WPI; 2002-608439/65 Strominger JL,

Example 1; Page 33; 54pp; English. encephalomyelitis.

New compositions comprising synthetic peptides in complex with a major histocompatibility complex class II HLADR2 protein, useful for treating a demyelinating disease, e.g. multiple sclerosis, or post-viral

The present invention describes compositions (I) comprising a peptide with an amino acid sequence with tyrosine (Y), lysine (K), and/or valine residues. The complex of the peptide with a major histocompatibility complex (MHC) class II HLA-DR2 protein is involved in modulating an

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immune response. (I) has antiinflammatory and neuroprotective activities, and can be used as AMC class II protein inhibitor. The compositions comprising the peptides are useful for treating demyelinating diseases such as multiple sclerosis, post-viral encephalomyelitis, a post-vaccine demyelinating condition, and a side effect of administering an antitumour necrosis factor agents. The peptide further inhibits proliferation of autoantigen-specific HAA-DRZ-restricted T cell clones ABP52207 to ABP52305 represent peptides used in the exemplification of the present
                                                                                                                                                                                                                                               invention
      888888888888888
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Sequence 15 AA;

Gaps ö Score 61; DB 5; Lengtn 10; Pred. No. 0.0039; '''-marches 1; Indels 1; Mismatches 74.4%; 86.7%; 13; Conservative Similarity Query Match Best Local 8 Best Loca Matches

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3 EKAKYEAYKAAAAA 17 1 EEAKYAAYKAAAAA 15 à g

RESULT 12

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0; Gaps

ABP52272 standard; peptide; 15 AA.

ABP52272;

16-OCT-2002 (first entry)

HLA-DR2 molecule binding peptide SEQ ID NO:66.

Human leukocyte antigen; HLA; major histocompatibility complex; MHC; HLA-DR2; MHC class II DR-2 molecule; demyelinating; multiple sclerosis; immune response; antiinflammatory; neuroprotective; proliferation; MHC class II protein inhibitor; demyelinating disease; inhibition; post-viral encephalomyelitis; post-vaccine demyelinating condition; anti-tumour necrosis factor agent.

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WO200259143-A2.

01-AUG-2002

24-JAN-2002; 2002WO-US002071.

24-JAN-2001; 2001US-0263569P.

(HARD) HARVARD COLLEGE

Strominger JL, Fridkis-Hareli M;

WPI; 2002-608439/65.

New compositions comprising synthetic peptides in complex with a major histocompatibility complex class II HLADR2 protein, useful for treating a demyelinating disease, e.g. multiple sclerosis, or post-viral encephalomyelitis.

Claim 28; Page 39; 54pp; English.

The present invention describes compositions (I) comprising a peptide with an amino acid sequence with tyrosine (Y), lysine (K), and/or valine residues. The complex of the peptide with a major histocompatibility complex (MHC) class II HIA-DR2 protein is involved in modulating an immune response. (I) has antiinflammatory and neuroprotective activities, and can be used as AMC class II protein inhibitor. The compositions comprising the peptides are useful for treating demyelinating diseases such as multiple sclerosis, post-viral encephalomyelitis, a post-vaccine demyelinating condition, and a side effect of administering an antitumour necrosis factor agents. The peptide further inhibits prolliferation of autoantigen-specific HLA-DR2-restricted T cell clones. ABP52207 to

Gaps

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Indels

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Mismatches

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13; Conservative

Matches

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Gaps

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The present invention describes compositions (I) comprising a peptide with an amino acid sequence with tyrosine (Y), lysine (K), and/or valine residues. The complex of the peptide with a major histocompatibility complex (MHC) class II HIA-DR2 protein is involved in modulating an immune response. (I) has antiinflammatory and neuroprotective activities, and can be used as a MHC class II protein inhibitor. The compositions comprising the peptides are useful for treating demyelinating diseases such as multiple sclerosis, post-viral encephalomyelitis, a post-vaccine demyelinating condition, and a side effect of administering an anti-tumour necrosis factor agents. The peptide further inhibits proliferation of autoantigen-specific HIA-DR2-restricted T cell clones. ABP52207 to ABP52305 represent peptides used in the exemplification of the present
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New compositions comprising synthetic peptides in complex with a major histocompatibility complex class II HLADR2 protein, useful for treating demyelinating disease, e.g. multiple sclerosis, or post-viral encephalomyelitis.
                                                                                                                                                                                                                                                                                                                                                                                                                                           HLA-DR2; MHC class II DR-2 molecule, demyelinating; multiple sclerosis; immune response; antihnflammatory; neuroprotective; proliferation; MHC class II protein inhibitor; demyelinating disease; inhibition; post-viral encephalomyelitis; post-vaccine demyelinating condition;
ABP52305 represent peptides used in the exemplification of the present
                                                                                                                                                                                                                                                                                                                                                                                                                            Human leukocyte antigen; HLA; major histocompatibility complex; MHC;
                                                                                                                         ö
                                                                                    Score 60; DB 5; Length 15; Pred. No. 0.0057; 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                        molecule binding peptide SEQ ID NO:53.
                                                                                                                                                                                                                                                                                 ABP52259 standard; peptide; 15 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Example 1; Page 33; 54pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 anti-tumour necrosis factor agent
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                                                                                                    86.78;
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                                                                                                                                                          3 EKAKYEAYKAAAAA 17
                                                                                                                                                                              (first entry)
                                                                                                                       13; Conservative
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                                                                                                      Local Similarity
                                                     Sequence 15 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 15 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WO200259143-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Strominger JL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     sapiens.
                                                                                                                                                                                                                                                                                                                                                       16-OCT-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-AUG-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Synthetic.
                                                                                                                                                                                                                                                                                                                    ABP52259;
                                                                                      Query Match
                                                                                                        Best Loca
Matches
                                                                                                                                                                                                                                              RESULT 13
ABP52259
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Score 59; DB 5; Length 15; Pred. No. 0.0083;

72.0%; 86.7%;

Query Match Best Local Similarity

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New compositions comprising synthetic peptides in complex with a major histocompatibility complex class II HLADR2 protein, useful for treating a demyelinating disease, e.g. multiple sclerosis, or post-viral encephalomyelitis.
                                                                                                                                                                                                                                                                      Human leukocyte antigen; HLA; major histocompatibility complex; MHC; HLA-DR2; MHC class II DR-2 molecule; demyelinating; multiple scletrosis; immune response; antinflammatory; neuroprotective; proliferation; MHC class II protein inhibitor; demyelinating disease; inhibition; post-viral encephalomyelitis; post-vaccine demyelinating condition;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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86.7%; Pred. No. 0.0083;
.ive 0; Mismatches 2;
                                                                                                                                                                                                                                  HLA-DR2 molecule binding peptide SEQ ID NO:51.
                                                                                                                                                                                                                                                                                                                                                                 anti-tumour necrosis factor agent.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Example 1; Page 32; 54pp; English.
                                                                                                                        ABP52257 standard; peptide; 15 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Fridkis-Hareli M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               24-JAN-2002; 2002WO-US002071.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   24-JAN-2001; 2001US-0263569P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EAAKYAAYKAAAAA 15
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                                                                                                                                                                                                  16-OCT-2002 (first entry)
3 EKAKYEAYKAAAAA
                                1 EKAAYAAYKAAAAA
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nes 13, Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2002-608439/65.
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                                                                                                                                                                                                                                                                                                                                                                                                                       Synthetic.
                                                                                                                                                              ABP52257;
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                                                                                        RESULT 14
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The present invention describes compositions (I) comprising a peptide with an amino acid sequence with tyrosine (Y), lysine (K), and/or valine residues. The complex of the peptide with a major histocompatibility complex (MHC) class II HIA-DEZ protein is involved in modulating an immune response. (I) has antiinflammatory and neuroprotective activities, and can be used as MHC class II protein inhibitor. The compositions comprising the peptides are useful for treating demyelinating diseases such as multiple sclerosis, post-viral encephalomyelitis, a post-vaccine demyelinating condition, and a side effect of administering an anti-tumour necrosis factor agents. The peptide further inhibits proliferation of autoantigen-specific HIA-DEZ-restricted T cell clones. ABBF52307 to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New compositions comprising synthetic peptides in complex with a major histocompastibility complex class II HLADR2 protein, useful for treating a demyelinating disease, e.g. multiple sclerosis, or post-viral encephalomyelitis.
                                                                                                                                                                                    Human leukocyte antigen; HLA; major histocompatibility complex; MHC; HLA-DR2; MHC class II DR-2 molecule; demyelinating; multiple sclerosis; immune response; antinflammatory; neuroprotective; proliferation; MHC class II protein inhibitor; demyelinating disease; inhibition; post-viral encephalomyelitis; post-vaccine demyelinating condition; anti-tumour necrosis factor agent.
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                                                                                                                                                   HLA-DR2 molecule binding peptide SEQ ID NO:91.
                                    ABP52297 standard; peptide; 15 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Fridkis-Hareli M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 28; Page 39; 54pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                    24-JAN-2002; 2002WO-US002071.
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                                                                                                              (first entry)
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                                                                                                              16-OCT-2002
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                                                                                                                                                                                                                                                                                                                                           Synthetic.
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RESULT 15
                     ABP52297
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Gaps

0

Search completed: March 31, 2005, 02:35:27 Job time: 100.629 secs

|| |:||||||| | EKPKFEAYKAAAAPA 15 3 EKAKYEAYKAAAAA 17

Local Similarity 80.0 1es 12; Conservative

Best Loca Matches

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Query Match 53.7%; Score 44; DB Best Local Similarity 68.8%; Pred. No. 28; Matches 11; Conservative 0; Mismatches
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ORGANISM: Rai
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US-09-732-210-1445
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US-08-836-620A-16
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18658, A
17859, A
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3, Appli
5, Appli
5, Appli
6, Appli
6, Appli
7, Appli
7, Appli
13950, A
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14713, A
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22139, A
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                                                                                          March 31, 2005, 02:26:53 ; Search time 26.0484 Seconds (without alignments) 48.718 Million cell updates/sec
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(cgn2_6/ptodata/1/iaa/5A_COMB.pep:*
(cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
(cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
(cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
(cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
(cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
(cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
          GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-08-836-620A-16
US-09-248-736-210-1445
US-09-248-766-17156
PCT-US95-04121-38
US-09-910-430-34
US-09-910-430-34
US-09-910-430-34
US-09-248-796A-17859
PCT-US94-10257A-33
US-09-248-796A-17859
PCT-US94-10257A-33
US-09-816-989A-3
US-09-816-989A-5
US-09-816-989A-6
US-09-816-989A-6
US-09-816-989A-7
US-09-816-289A-7
US-09-117-121-16
US-09-117-121-24
US-09-117-121-24
US-09-2152-291A-22139
US-09-2052-291A-22139
US-09-2052-291A-22139
                                                                                                                                                                                                                                                                                   Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                          513545 segs, 74649064 residues
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                                                                                                                                                                                                                                                                                                                                                          Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                - protein search, using sw model
                                                                                                                                                                                                                BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                   1 APEKAKYEAYKAAAAA 17
                                                                                                                                                      US-10-056-583A-88
82
                                                                                                                                                                                                                                                                                                                   seq length: 0
seq length: 200000000
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Match ]
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                                                                                                                                                     Title:
Perfect score:
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Maximum DB
                                                                                                                                                                                    Sequence:
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                                                                                               Run on:
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No.
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sequence 28, Appl
Sequence 11242, A
Sequence 45793, A
Sequence 652, Arrised
                                                                   Sequence 4, Appli
Sequence 21824, A
Sequence 18769, A
Sequence 5116, Ap
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Sequence
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Sequence
Sequence
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 Seguence
                                                                                                                                                                                                                                                                                                             Seguence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION: Orphan receptor
NUMBER OF SEQUENCES: 19
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/836,620A
FILING DATE:
           US-09-248-796A-18456
US-08-295-670-6
US-08-633-485-6
US-08-508-7618-4
US-09-525-991A-18769
US-09-552-991A-18769
US-09-543-681A-5116
US-09-117-11-3
US-08-245-511-2
US-08-245-511-2
US-08-245-511-2
US-08-245-511-2
US-09-902-540-11242
US-09-912-540-11242
US-09-118-45793
US-09-138-452A-652
                                                                                                                                                                                                                                                                                                                                                                ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/EP96/03933
FILING DATE: 08-SEP-1995
PRIOR APPLICATION NUMBER: GB 9518272.1
FILING DATE: 08-SEP-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9605550.4
FILING DATE: 15-MAR-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9607532.0
FILING DATE: 11-APR-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9609576.5
FILING DATE: 08-MAY-1996
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 596 anino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; Sequence 16, Application US/08836620A; Patent No. 5958710; GENERAL INFORMATION:
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Gaps

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Length 596 Indels

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Sequence 14713, Application US/09902540

Patent No. 6833447

GENERAL INFORMATION:
APPLICANT: Goldman, Barry S.
APPLICANT: Blater, Steven C.
APPLICANT: Missand, Roger C.
TILE REPERENCE: 38-10(15849)B

CURRENT APPLICATION NUMBER: US/09/902,540

CURRENT FAPLICATION NUMBER: 00/217,883

FRIOR APPLICATION NUMBER: 60/217,883

FRIOR APPLICATION NUMBER: 60/217,883

FRIOR FILING DATE: 2000-07-10

NUMBER OF SEQ ID NOS: 16825

SEQ ID NO 14713
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                           SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO) CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/04121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 42; DB 5
Pred. No. 0.93;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1; Mismatches
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                                                                                                                                                                                                                    NAME: Vanstone, Darlene A.
REGISTRATION NUMBER: 35,279
REFERNICE/DOCKET NUMBER: 079.2PCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 466-6010
INFORMATION FOR SEQ ID NO: 38:
SEQUENCE CHARACTERISTICS:
         PC-DOS/MS-DOS
                                                                                                              CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE: April 1, 1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 34, Application US/09910430; Patent No. 6794166; GENERAL INFORMATION: APPLICANT: Godfroi, Edmond; APPLICANT: Bollen, Alex
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         51.2%;
76.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: PRT ORGANISM: Myxococcus xanthus
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120 APERTEYRVWRAAA 133
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                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: amino acid
STRANDENNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
FRAGMENT TYPE: internal
                                                                                                                                                                                                                                                                                                                                                                                                      13 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 76.9
Matches 10; Conservative
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1 AAYKAAKAAAAAA 13
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Matches 7; Conservative
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US-09-902-540-14713
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                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH:
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Sequence 17156, Application US/09248796A
Sequence 17156, Application US/09248796A
Sequence 17156, Application US/09248796A
Sequence 17156, Application US/09248796A
Sequence 17156
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                                                          APPLICANT: Bunkers, Greg J.
APPLICANT: Liang, Jihong
APPLICANT: Liang, Jihong
APPLICANT: Liang, Jihong
APPLICANT: Liang, Jihong
APPLICANT: Mittanck, Cindy A.
APPLICANT: Wu, Younie S.
TITLE OF INVENTION: Anti-fungal Proteins and Methods for Their Use
FILE REFERENCE: 38-21(15036)8
CURRENT APPLICATION NUMBER: US/09/732,210
FRIOR APPLICATION NUMBER: US 60/169,513
PRIOR APPLICATION NUMBER: US 60/169,340
PRIOR PILING DATE: 1999-12-07
PRIOR PILING DATE: 1999-12-07
NUMBER OF SEQ ID NOS: 1753
SEQ ID NO 1445
LENGTH: 162
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     52.4%; Score 43; DB 4; Length 162; 52.9%; Pred. No. 9.9;
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Pred. No. 21;
1; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT:
TITLE OF INVENTION: Haptenated Peptides and Uses Thereof
NUMBER OF SEQUENCES: 62
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches
Sequence 1445, Application US/09732210
Patent No. 6573361
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                   , ORGANISM: Mycobacterium tuberculosis
US-09-732-210-1445
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97 APKPSKLEVFNAALAAA 113
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Best Local Similarity 71.4%;
Matches 10; Conservative
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ORGANISM: Candida albicans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
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Best Local Similarity
The 9; Conserve
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PCT-US95-04121-38
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APPLICANT: BRIGITTE DEVAUX
APPLICANT: JONATHAN B. ROTHBARD
TITLE OF INVENTION: GLYCOPROTEIN AND PEPTIDE PORTIONS THEREOF IN PROTOCOLS
TITLE OF INVENTION: RELATED TO AUTOIMMUNE DISEASE
NUMBER OF SEQUENCES: 95
CORRESPONDENCE ADDRESS:
ADDRESSEE: IMMULOGIC PHARMACEUTICAL CORPORATION
STREET: 610 LINCOLN STREET
                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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0
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Pred. No. 2;
0; Mismatches
                                                                                                                                                                                                                                                                   Score 41; DB 4
Pred. No. 57;
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: ASCII text
CURRENT APPLICATION DATA:
PAPLICATION NUMBER: PCT/US94/10257A
FILING DATE: 1 SEPTEMBER 1994
                    PRIOR APPLICATION NUMBER: US 60/074,725
PRIOR FILING DATE: 1998-02-13
PRIOR APPLICATION NUMBER: US 60/096,409
PRIOR FILING DATE: 1998-08-13
NUMBER OF SEQ ID NOS: 28208
SEQ ID NO 17859
LENGTH: 402
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: ANNE I CRAIG
REGISTRATION NUMBER: 32,976
REFERENCE/DOCKET NUMBER: 071.1 PCT
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 33, Application PC/TUS9410257A GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/116,824
FILING DATE: 03-SEP-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
         CURRENT FILING DATE: 1999-02-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEFAX: (617) 466-6040 INFORMATION FOR SEQ ID NO: 33: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (617) 466-6000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  48.8%;
                                                                                                                                                                                                                                                                   50.0%;
80.0%;
                                                                                                                                                                             ; TYPE: PRT
; ORGANISM: Candida albicans
US-09-248-796A-17859
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Best Local Similarity 76.9
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                             8; Conservative
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Best Local Similarity
Matches 8; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CITY: WALTHAM
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Patent No. 6747137
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
CURRENT APPLICATION NUMBER: US/09/248,796A
CURRENT FILING DATE: 1999-02-13
PRIOR APPLICATION NUMBER: US 60/074,725
PRIOR APPLICATION NUMBER: US 60/096,409
PRIOR PILING DATE: 1998-08-13
NUMBER OF SEQ ID NOS: 28208
SEQ ID NO 18656
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
APPLICANT: Keith Weinstock et al
TITLE OF INVENTION: VUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN
TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.132
CURRENT APPLICATION NUMBER: US/09/248,796A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            . LOCATION: (21)
; OTHER INFORMATION: Identity of amino acid sequences at the above locations are unkno
US-09-248-796A-18658
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APPLICANT: Leboulle, Gerard
TITLE OF INVENTION: IDENTIFICATION AND MOLECULAR CHARACERIZATION OF
TITLE OF INVENTION: PROTEINS, EXPRESSED IN THE IXODES RICINUS SALIVARY
TITLE OF INVENTION: GLANDS
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Pred. No. 1.1e+02;
0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                   DB 4; Length 273;
26;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                7; Indels
                                                                              TILE REFERENCE: VANM229,001CP1
CURRENT APPLICATION NUMBER: US/09/910,430
CURRENT FILING DATE: 2001-07-19
FRIOR RPLICATION NUMBER: PCT/BE00/00061
PRIOR PILING DATE: 2000-06-06
PRIOR FILING DATE: 1999-06-09
NUMBER OF SEQ ID NOS: 34
SOFTWARE: PSESEQ for Windows Version 3.0
SSOFTWARE: 273
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                                                                                                                                                                                                                                                                                                                                                                                                                     Score 42;
Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                                     51.2%;
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Best Local Similarity 78.6%;
Matches 11; Conservative
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                                                                                                                                                                                                                                                                                                                             ; TYPE: PRT
; ORGANISM: Ixodes ricinus
US-09-910-430-34
                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
Matches 9; Conserv
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US-09-248-796A-18658
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APPLICANT: Gad, Alexander
APPLICANT: Gad, Alexander
APPLICANT: Lis, Doris
APPLICANT: Lis, Doris
APPLICANT: Lis, Doris
TITLE OF INVENTION: COPOLYMER I RELATED POLYPEPTIDES FOR USE AS MOLECULAR WEIGHT MARKI
TITLE OF INVENTION: AND FOR THERAPEUTIC USE
FILE REFERENCE: 2609/60807-A-PCT-US
CURRENT APPLICATION NUMBER: US/09/816,989A
CURRENT FILING DATE: 2001-03-23
PRIOR APPLICATION NUMBER: 60/101,693
PRIOR APPLICATION NUMBER: PCT/US99/22402
PRIOR APPLICATION NUMBER: PCT/US99/22402
PRIOR PILING DATE: 1999-09-24
NUMBER OF SEQ ID NOS: 7
SOFTWARE: Patentin version 3.1
SEQ ID NO 5
LENGTH: 77
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
GENERAL INFORMATION:

APPLICANT: Yeda Research and Development Co., Ltd.

TITLE OF INVENTION: GLATIRAMER ACETATE MOLECULAR WEIGHT MARKERS FILE REFERENCE: 60807-A

CURRENT APPLICATION NUMBER: US/09/405,743A

CURRENT FILING DATE: 1999-09-24

NUMBER OF SEQ ID NOS: 7

SEQ ID NO 5

LENGTH: 77
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TITLE OF INVENTION: GLATIRAMER ACETATE MOLECULAR WEIGHT MARKERS
FILE REFERENCE: 60807-A
CURRENT APPLICATION NUMBER: US/09/405,743A
CURRENT FILING DATE: 1999-09-24
NUMBER OF SEQ ID NOS: 7
SOFTWARE: PatentIn Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
48.8%; Score 40; DB 4; Length 77;
Best Local Similarity 60.0%; Pred. No. 14;
Matches 9; Conservative 3; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 48.8%; Score 40; DB 4; Length 77; Best Local Similarity 60.0%; Pred. No. 14; Matches 9; Conservative 3; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                             ; OTHER INFORMATION: Description of Artificial Sequence:
; OTHER INFORMATION: PEPTIDE
US-09-405-743A-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 5, Application US/09816989A Patent No. 6800287
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                                                                                                                                                                                                                                                                   TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: PRT ORGANISM: Artificial Sequence
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18 AAKKAEAKAYKAAEA 32
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18 AAKKAEAKAYKAAEA 32
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US-09-816-989A-5
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US-09-405-743A-6
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APPLICANT: Gad, Alexander
APPLICANT: Lis, Decander
TITLE OF INVENTION: COPOLYMER I RELATED POLYPEPTIDES FOR USE AS MOLECULAR WEIGHT MARK
TITLE OF INVENTION: AND FOR THERAPEUTIC USE
FILE REFERENCE: 2609/60807-A-PCT-US
CURRENT APPLICATION NUMBER: US/09/816,989A
CURRENT APPLICATION NUMBER: 0/101,693
PRIOR APPLICATION NUMBER: PCT/US99/22402
PRIOR FILING DATE: 1998-09-25
PRIOR FILING DATE: 1999-09-24
NUMBER OF SEQ ID NOS: 7
SOFTWARE: Patentin version 3.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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                                                                                                                           US-09-405-743A-3

Sequence 3, Application US/09405743A

Patent No. 651493B

GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: GLATIRAMER ACETATE MOLECULAR WEIGHT MARKERS
FILE REFERENCE: 60807-A

CURRENT APPLICATION UNBER: US/09/405,743A

CURRENT FILING DATE: 1999-09-24

NUMBER OF SEQ ID NOS: 7

SOFTWARE: Patentin Ver. 2.1

SEQ ID NO 3

LENGTH: 56
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88.8%; Score 40; DB 4; Length 56;
Best Local Similarity 60.0%; Pred. No. 9.7;
Matches 9; Conservative 3; Mismatches 3; Indels
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Pred. No. 9.7;
3; Mismatches 3; Indels
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US-09-816-989A-3
; Sequence 3, Application US/09816989A
; Patent No. 6800287
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: PRT
ORGANISM: Artificial Sequence
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Best Local Similarity 60.0%;
Matches 9; Conservative
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18 AAKKAEAKAYKAAEA 32
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18 AAKKAEAKAYKAAEA 32
                        1 AAYAAKAAAAA 13
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US-09-405-743A-5
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Sequence of Application US/09816989A

Sequence of Application US/09816989A

Sequence of Application US/09816989A

Setent No. 6800287

GENERAL INFORMATION:

APPLICANT: dis, Doris

TITLE OF INVENTION: COPOLYMER 1 RELATED POLYPEPTIDES FOR USE AS MOLECULAR WEIGHT MARK

TITLE OF INVENTION: AND FOR THERAPEUTIC USE

TITLE OF INVENTION AND FOR THERAPEUTIC USE

TITLE OF INVENTION AND FOR THERAPEUTIC USE

TITLE OF INVENTION AND FOR THERAPEUTIC USE

FILE REPERENCE: 2609/60807-A-PCT-US

CURRENT APPLICATION NUMBER: 6/101,693

PRIOR PELLING DATE: 1998-09-25

PRIOR APPLICATION NUMBER: PCT/US99/22402

PRIOR APPLICATION NUMBER: PCT/US99/22402

NUMBER OF SEQ ID NOS: 7

SOFTWARE: PATENTING DATE: 1999-09-34

NUMBER OF SEQ ID NOS: 7

SEG ID NO 6

LENGTH: 86
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// OTHER INFORMATION: Description of Artificial Sequence: Synthetic Peptide

US-09-816-989A-6
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; SEQ ID NO 6

; LENGTH: 86

; TYPE: PRT

; ORGANISM: Attificial Sequence
; CRATURE:
; OTHER INFORMATION: DESCRIPTION
; OTHER INFORMATION: PEPTIDE
US-09-405-743A-6
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48.8%; Score 40; DB 4; Length 86;
Best Local Similarity 60.0%; Pred. No. 16;
Matches 9; Conservative 3; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 48.8%; Score 40; DB 4; Length 86; Best Local Similarity 60.0%; Pred. No. 16; Matches 9; Conservative 3; Mismatches 3; Indels
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ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                  1 APEKAKYEAYKAAAA 15
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18 AAKKAEAKAYKAAEA 32
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US-09-816-989A-6
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Db 18 AAKKAEAKAYKAABA 32

Search completed: March 31, 2005, 02:44:08 Job time : 27.0484 secs

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March 31, 2005, 02:29:23 ; Search time 75.4032 Seconds (without alignments) 74.648 Million cell updates/sec
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/cgn2_6/ptodata/2/pubpaa/US11_NEW_PUB.pep.*
/cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep.*
/cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep.*
GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
                                                            - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                    1 APEKAKYEAYKAAAAA 17
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82
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Maximum DB seq length: 2000000000
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Sequence:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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		* Query	* Query				
No.	Score	Match	Length	BB	ID	Description	
;	82	100.0	17	14	US-10-056-583-88	Sequence 88,	Appl
	82	100.0	19	14	US-10-056-583-89	Sequence 89,	Appl
٠	73	89.0	17	14	US-10-056-583-97	Sequence 97,	Appl
	71	9.98	15	14	US-10-056-583-65	Sequence 65,	Appl
	71	9.98	17	14	US-10-056-583-90	Sequence 90,	Appl
	69	84.1	17	14	US-10-056-583-96	Seguence 96,	Appl
	65	79.3	15	14	US-10-056-583-64	Sequence 64,	Appl
	63	76.8	15	14	US-10-056-583-95	Seguence 95,	Appl
	62	75.6	15	14	US-10-056-583-92	Sequence 92,	Appl
_	61	74.4	15	14	US-10-056-583-57	Sequence 57,	Appl
	61	74.4	15	14	US-10-056-583-85	Sequence 85,	Appl
	9	73.2	15	14	US-10-056-583-66	Sequence 66,	Appl
	59	72.0	15	14	US-10-056-583-51	Sequence 51,	Appl

	23,		33,	45,	47,	38,		56,	63,	84,	86,	30,	58,	61,	93,	29,	equence 34,	35,	42,	43,	equence 48,	equence 49,	98,	equence 25,	equence 26,	62,	311	2514	29,	44,	Sequence 32, Appl	37,
	-10-056-583-5	-10-056-583-9	10-056-58	-10-056-583-4	-10-056-583-4	-10-056-583-3	-10-056-583-	-10-056-583-5	-10-056-583-6	-10-056-583-8	-10-056-583-8	-10-056-583-3	-10-056-583-5	-10-056-583-6	-10-056-583-9	-10-056-583-5	-10-056-583-3	-10-056-583-3	-10-056-58	10-056-583-4	-10-056-583-4	-10-056-583-4	-10-056-583-9	-10-056-583-2	-10-056-583-2	-10-056-583-6	-10-094-	-10-408-765A-2	-10-056-583-2	-10-056-583-4	9-5	-10-056-583-3
	14	14	14	14	14	14	14	14	14	14	14	14	14	14	14	14	14	14	14	14	14	14	14.	14	14	14		16	14	14	14	14
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ALIGNMENTS

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US-10-056-583-88

i Sequence 88, Application US/10056583

j Sequence 88, Application US/10056583

j Republication No. US20030064915A1

GENERAL INFORMATION:

APPLICANT: Presidents and Fellows of Harvard College

APPLICANT: Presidents and Fellows of Harvard College

APPLICANT: Presidents and Fellows of Harvard College

APPLICANT: Pridkis-Hareli, Masha

i TITLE OF INVENTION: CONDITIONS

FILE REFERENCE: 24655-017

CURRENT APPLICATION NUMBER: US/10/056,583

FILE REFERENCE: 2002-01-24

PRIOR PLLING DATE: 2001-01-24

PRIOR FILING DATE: 2001-01-24

PRIOR FILING DATE: 2001-01-24

NUMBER OF SEQ ID NOS: 99

SOFTWARE: FRACTOR: 17

TYPE: PRT

CORGANTS: 17

TYPE: PRT

CORGANTS: 17

TYPE: PRT

TYPE: PRT

ORGANTS: 17

TYPE: PRT

ORGANTS: 100.0%; Score 82; DB 14; Length 17;

Best Local Similarity 100.0%; Pred: No: 1.6e-06;

Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps

ON

1 APEXAKYERAYKAAAAAA 17

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1 APEXAKYERAYKAAAAAA 17

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1 APEXAKYERAYRAAAAA 17
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Db 1 APEKAKYEAYKA RESULT 2 US-10-056-583-89

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GENERAL INFORMATION:
APPLICANT: Presidents and Pellows of Harvard College
APPLICANT: Strominger, Jack L.
APPLICANT: Strominger, Jack L.
TITLE OF INVENTION: TRERAPEDTIC PEPTIDES FOR DEMYELINATING
TITLE OF INVENTION: CONDITIONS
FILE REFERENCE: 24655-017
CURRENT APPLICATION NUMBER: 60/26,583
CURRENT APPLICATION NUMBER: 60/263,569
PRIOR FILING DATE: 2001-01-24
NUMBER OF SEQ ID NOS: 99
SOFTWARE FRAEER (FALMON NUMBER: 60/263,569
FRIOR FILING DATE: 2001-01-24
SOFTWARE FRAEER (FALMON NUMBER: 60/263,569
FRIOR FILING DATE: 2001-01-24
SOFTWARE FRAEER (FALMON NUMBER: FALMON NUMBER (FALMON NUMBER)
FRIOR FILING DATE: 2001-01-24
SOFTWARE FRAEER (FALMON NUMBER)
FRIOR FILING DATE: 2001-01-24
SOFTWARE (FALMON NUMBER)
FRIOR FILING DATE: 2001-01-34
; APPLICANT: Fridkis-Hareli, Masha; TITLE OF INVENTION: THERAPEUTIC PEPTIDES FOR DEMYELINATING; TITLE OF INVENTION: THERAPEUTIC PEPTIDES FOR DEMYELINATING; TITLE OF INVENTION: CONDITIONS; FILE REFERENCE: 24655-017; CURRENT FILIATION NUMBER: US/10/056,583; CURRENT FILIATION NUMBER: 00/263,569; PRIOR APPLICATION NUMBER: 2001-01-24; NUMBER OF SEQ ID NOS: 99; SCOPTWARR: FABELSEQ for Windows Version 4.0; SEQ ID NO 65; LENGTH: 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                         FEATURE:
; OTHER INFORMATION: The peptide was designed and synthesized
US-10-056-583-65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              , OTHER INFORMATION: The peptide was designed and synthesized US-10-056-583-90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 15;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 14; L 9.8e-05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        86.6%; Score 71; DB 14; I
100.0%; Pred. No. 8.6e-05;
tive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-10-056-583-90
; Sequence 90, Application US/10056583
; Publication No. US20030064915A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 96, Application US/10056583; Publication No. US20030064915A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3 EKAKYEAYKAAAAA 17
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Best Local Similarity 100.
Matches 15; Conservative
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                                                                                      APPLICANT: Presidents and Fellows of Harvard College
APPLICANT: Strominger, Jack L.
APPLICANT: Strominger, Jack L.
TITLE OF INVENTION: THERAPEUTIC PEPTIDES FOR DEMYELINATING
TITLE OF INVENTION: CONDITIONS
FILE REPERBENCE: 24655-017
CURRENT APPLICATION NUMBER: 60/26,583
CURRENT FILING DATE: 2002-01-24
PRIOR PELING DATE: 2001-01-24
NUMBER OF SEQ ID NOS: 99
SOFTWARE: FastSEQ for Windows Version 4.0
LENGTH: 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 97, Application US/10056583;
Publication No. US20030064915A1;
GENERAL INFORMATION:
APPLICANT: Presidents and Fellows of Harvard College;
APPLICANT: Strominger, Jack L.
TITLE OF INVENTION: THERAPEUTIC PEPTIDES FOR DEMYELINATING
TITLE OF INVENTION: CONDITIONS;
FILE REFERENCE: 24655-017
CURRENT APPLICATION NUMBER: US/10/056,583
CURRENT FILING DATE: 2002-01-24
PRIOR PILING DATE: 2001-01-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; OTHER INFORMATION: The peptide was designed and synthesized US-10-056-583-89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 19;
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US-10-056-583-65
; Sequence 65, Application US/10056583
; Publication No. US20030064915A1
; GENERAL IMPORMATION:
; APPLICANT: Presidents and Fellows of Harvard College
; APPLICANT: Strominger, Jack L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 100.0%; Pred. No. 1.8e-06;
Matches 17; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQ ID NOS: 99
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 97
LENGTH: 17
      Sequence 89, Application US/10056583
Publication No. US20030064915A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 APEKAKYEAYKAAAAA 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 APEKAKFEAYKAAAAPA 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APEKAKYEAYKAAAAA 17
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ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: PRT ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     15; Conservative
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Matches 15; Conserv
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US-10-056-583-97
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TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
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Best Local Similarity 86.7%;
Matches 13; Conservative
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                                                                                                                                                                                                                                                                                            3 EKAKYEAYKAAAAA 17
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity 93.3
Matches 14; Conservative
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  SEQ ID NO 95
LENGTH: 15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Strominger, Jack L.
APPLICANT: Strominger, Jack L.
TITLE OF INVENTION: THERABEUTIC PEPTIDES FOR DEMYELINATING
TITLE OF INVENTION: CONDITIONS
FILE REFERENCE: 24655-017
CURRENT APPLICATION NUMBER: US/10/056,583
CURRENT FILING DATE: 2002-01-24
PRIOR FILING DATE: 2001-01-24
PRIOR FILING DATE: 2001-01-24
NUMBER OF SEQ ID NOS: 99
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
APPLICANT: Presidents and Fellows of Harvard College
APPLICANT: Presidents and Fellows of Harvard College
APPLICANT: Stroninger, Jack L.
APPLICANT: Fridiia-Hareli, Masha
TITLE OF INVENTION: THERAPEUTIC PEPTIDES FOR DEMYELINATING
TITLE OF INVENTION: CONDITIONS
FILE REPRENCE: 24655-017
CURRENT APPLICATION NUMBER: 60,265,583
CURRENT APPLICATION NUMBER: 60,263,569
PRIOR APPLICATION NUMBER: 60,263,569
PRIOR FILING DATE: 2001-01-24
NUMBER OF SEQ ID NOS: 99
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                   ; OTHER INFORMATION: The peptide was designed and synthesized.
US-10-056-583-96
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; OTHER INFORMATION: The peptide was designed and synthesized.
US-10-056-583-64
                                                                                                                                                                                                                                                                                     84.1%; Score 69; DB 14; Length 17; 82.4%; Pred. No. 0.00021; tive 2; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            79.3%; Score 65; DB 14; Length 15; 93.3%; Pred. No. 0.00081; ive 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 64, Application US/10056583
Publication No. US20030064915A1
GENERAL INFORMATION:
APPLICANT: Presidents and Fellows of Harvard College
CURRENT FILING DATE: 2002-01-24
PRIOR APPLICATION NUMBER: 60/263,569
PRIOR FILING DATE: 2001-01-24
NUMBER OF SEQ ID NOS: 99
SOFTWARE: FASISEQ for Windows Version 4.0
SEQ ID NO 96
LENGTH: 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; Sequence 95, Application US/10056583; Publication No. US20030064915A1
                                                                                                                                                                                                                                                                                                                                                                                                   1 APEKAKFEAFKAAAAPA 17
                                                                                                                                                                                                                                                                                                                                                                            1 APEKAKYEAYKAAAAA 17
                                                                                                                                                        TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: PRT
ORGANISM: Artificial Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 93.33,
Best Local 14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 EAAKYEAYKAAAAA 15
                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 82.4
Matches 14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 7
US-10-056-583-64
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| Marches | 15 | March | 15 | Marches | 15 | Marches | 15 | March | 15
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; OTHER INFORMATION: The peptide was designed and synthesized.
US-10-056-583-53
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                                                                                                                                                                                                                                                                   APPLICANT: Strominger, Jack L.
APPLICANT: Strominger, Jack L.
APPLICANT: Fridkis-Hareli, Macha
TITLE OF INVENTION: THERAPUTIC PEPTIDES FOR DEMYELINATING
TITLE OF INVENTION: CONDITIONS
FILE REFERENCE: 24655-017
CURRENT APPLICATION NUMBER: US/10/056,583
CURRENT FILING DATE: 2002-01-24
PRIOR APPLICATION NUMBER: 60/263,569
PRIOR FILING DATE: 2001-01-24
          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2; Indels
                                                                                                                                                                                       Sequence 51, Application US/10056583
Publication No. US20030064915A1
GENERAL INFORMATION:
APPLICANT: Presidents and Pellows of Harvard College
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 59; DB 14;
Pred. No. 0.0076;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 59; DB 14;
Pred. No. 0.0076;
            Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Mismatches
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 51
LENGTH: 15
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86.7%;
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86.7%;
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ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORGANISM: Artificial Sequence
                                                   3 EKAKYEAYKAAAAA 17
                                                                                        1 EAKKYEAYKAAAAA 15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3 EKAKYEAYKAAAAA 17
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Best Local Similarity 86.73
Matches 13; Conservative
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Best Local Similarity 86.7
Matches 13; Conservative
          13; Conservative
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            Matches
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0
; OTHER INFORMATION: The peptide was designed and synthesized.
US-10-056-583-57
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            74.4%; Score 61; DB 14; Length 15; illarity 86.7%; Pred. No. 0.0036; Conservative 0; Mismatches 2: Indele
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               73.2%; Score 60; DB 14; Length 15; 86.7%; Pred. No. 0.0052;
                                                                        Length 15
                                                                                                                                                                                                                                                               US-10-056-583-85

Sequence 85, Application US/10056583

Sequence 85, Application US/10056583

GENERAL INFORMATION:

APPLICANT: Presidents and Fellows of Harvard College
APPLICANT: Strominger, Jack L.

APPLICANT: Frickis-Hareli, Masha
TITLE OF INVENTION: THERAPEUTIC PEPTIDES FOR DEMYELINATING

TITLE OF INVENTION: CONDITIONS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Strominger, Jack L.
PEDLICANT: Fridkts-Harell, Masha
TITLE OF INVENTION: THERAPEUTIC PEPTIDES FOR DEMYELINATING
TITLE OF INVENTION: CONDITIONS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 66, Application US/10056583
Publication No. US20030064915A1
GENERAL INFORMATION:
APPLICANT: Presidents and Fellows of Harvard College
                                                                   Score 61; DB 14;
Pred. No. 0.0036;
                                                                                                           Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                            FILE REFERENCE: 24655-017
CURRENT APPLICATION NUMBER: US/10/056,583
CURRENT FILING DATE: 2002-01-24
PRIOR APPLICATION NUMBER: 6/263,569
PRIOR FILING DATE: 2001-01-24
NUMBER OF SEQ ID NOS: 99
SOFTWARE: PastSEQ for Windows Version 4.0
SEQ ID NO 85
LENGTH: 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQ ID NOS: 99
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 66
LENGTH: 15
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CURRENT APPLICATION NUMBER: US/10/056,583
CURRENT FILING DATE: 2002-01-24
PRIOR APPLICATION NUMBER: 60/263,569
PRIOR PILING DATE: 2001-01-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: PRT
ORGANISM: Artificial Sequence
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ORGANISM: Artificial Sequence
                                                                   Query Match
Best Local Similarity 86.7%;
Matches 13; Conservative
                                                                                                                                                    3 EKAKYEAYKAAAAA 17
                                                                                                                                                                                       1 EEAKYAAYKAAAAA 15
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Best Local Similarity
Matches 13; Conserv
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Best Local Similarity
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RESULT 15
US-10-056-583-91
Sequence 91, Application US/10056583
Sequence 91, Application US/10056583
Publication No. US20030064915A1
GENERAL INFORMATION:
APPLICANT: Strominger, Jack L.
APPLICANT: Fridkis-Hareli, Masha
TITLE OF INVENTION: CONDITIONS
FILE OF INVENTION: CONDITIONS
FILE REPERENCE: 24655-017
CURRENT APPLICATION NUMBER: US/10/056,583
CURRENT FILING DATE: 2002-01-24
PRIOR PILING DATE: 2001-01-24
NUMBER OF SEQ ID NOS: 99
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 91
LENGTH: 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: PRT:
ORGANISM: Artificial Sequence
PREATURE:
COTHER INFORMATION: The peptide was designed and synthesized.
US-10-056-583-91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 80.0%; Pred. No. 0.016;
Matches 12; Conservative 1; Mismatches 2; Indels
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1 EKPKFEAYKAAAAPA 15 g

3 EKAKYEAYKAAAAA 17

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Search completed: March 31, 2005, 02:48:48 Job time: 75.4032 secs

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5.1.6
Compugen Ltd.
version 5
GenCore
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OM protein - protein search, using sw model

March 31, 2005, 02:26:17; Search time 20.2903 Seconds (without alignments) 80.614 Million cell updates/sec Run on:

1 APEKAKYEAYKAAAAA 17 US-10-056-583A-88 82 Perfect score: Sequence: Title:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283416 seqs, 96216763 residues Searched:

283416 Total number of hits satisfying chosen parameters:

seq length: 0 seq length: 200000000 Minimum DB Maximum DB

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database

PIR_79:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Description	conserved hypothet	conserved hypothet	50S ribosomal prot	50S ribosomal prot	~		estrogen receptor			T-cell receptor da		peptidyl-prolyl ci	tolA protein - Esc	GAP-43-related pro	homeotic protein H	homeotic protein H	hypothetical prote	DNA polymerase III	DNA polymerase III	transcription fact	trans-activating t	peptidyl methionin	peptidyl methionin	probable 14-3-3 pr	hypothetical prote	FL-160-4 protein -	fatty-acid synthas	hypothetical prote	phd protein - phag
SUMMAKIES	ID	H81076	B81866	F97683	AF2908	877930	877935	QRMSE	QRRTE	H70927	836290	A81794	B81216	JV0057	A43555	I50145	A43562	D96030	D97516	AD2735	JC2184	TNLJG3	AD1307	AD1679	H86355	AC1399	PH1919	JC4086	T27431	S40015
	DB	~	~	N	~	7	~	7	-	7	7	~	~	~	~	N	7	~	~	~	~	-	~	7	7	N	~	-	7	7
	Query Match Length	154	154	179	179	189	189	599	600	162	185	347	348	421	441	188	289	329	1167	1167	88	129	177	177	254	289	641	1885	2129	73
de	Query Match	 54.9	54.9	54.9	54.9	54.3	54.3	53.7	53.7	52.4	52.4	52.4	52.4	52.4	52.4	51.2	51.2	51.2	51.2	51.2	50.0	50.0	20.0	50.0	50.0	50.0	50.0	50.0	50.0	48.8
	Score	 45	45	45	45	44.5	44.5	44	44	43	43	43	43	43	43	42	42	42	42	42	41	41	41	41	41	41	41	41	41	40
	Result No.	 -	7	٣	4	S	9	7	80	σ	10	11	12	13	14	15	16	17	18	19	50	21	22	23	24	25	56	27	28	29

M-like protein enn	trans-activating t	hypothetical prote	probable transcrip	probable fatty-aci	hypothetical prote	H+-transporting tw	conserved hypothet	hypothetical prote	hypothetical prote	translation initia	CT147 hypothetical	conserved hypothet	ct147 hypothetical	probable fatty-aci	fatty acid synthas
S61806	TNLJS2	AB3271	A83492	T43037	AC2015	804675	G70302	T50013	T13690	E64114	F86509	C81558	H72112	T43409	T38781
7	٦	0	~	~	7	7	7	N	~	~	N	~	~	N	7
75	106	101	202	377	467	478	480	594	806	829	1537	1537	1537	1842	1842
48.8	48.8	48.8	48.8	48.8	48.8	48.8	48.8	48.8	48.8	48.8	48.8	48.8	48.8	48.8	48.8
40	40	40	40	40	40	40	40	40	40	40	40	40	40	40	40
30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

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žES	181

Conserved hypothetical protein NMB1500 [imported] - Neisseria meningitidis (strain MC58 C;Species: Neisseria meningitidis
C;Species: Neisseria meningitidis
C;Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 09-Jul-2004
C;Accession: HB1076
R;Tettelin, H.; Saunders, N.J.; Heidelberg, J.; Jeffries, A.C.; Nelson, K.E.; Eisen, J.A. Hickey, E.K.; Haft, D.H.; Salzberg, S.L.; White, O.; Fleischmann, R.D.; Dougherty, B.A.; ri, H.; Oin, H.; Vanathevan, J.; Gill, J.; Scarlato, V.; Masignani, V.; Pizza, M. Science 287, 1809-1815, 2000
A;Authors: Grandl, G.; Sunt, L.; Smith, H.O.; Fraser, C.M.; Moxon, E.R.; Rappuoli, R.; Ve A;Title: Complete genome sequence of Neisseria meningitidis serogroup B strain MC58.
A;Reference number: A81000; MUID:20175755; PMID:10710307
A;Scatus: preliminary
A;Molecule type: DNA
A;Residues: 1-154 «TETA
A;Cross-references: UNIPROT:Q9JYN4; GB:AE002499; GB:AE002098; NID:g7226737; PIDN:AAF4185
A;Experimental source: serogroup B, strain MC58

A,Gene: NMB1500 C,Superfamily: Escherichia coli ybdQ protein

Gaps ö 54.9%; Score 45; DB 2; Length 154; 56.2%; Pred. No. 5.4; '4; Aismatches 3; Indels Conservative Query Match Best Local Similarity Matches 9; Conserv

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RESULT 2

Conserved hypothetical protein NWA1703 [imported] - Neisseria meningitidis (strain 22491 Cispecies: Neisseria meningitidis
Cispecies: Neisseria meningitidis
Cipate: 05-May-2000 #sequence_revision '05-May-2000 #text_change 09-Jul-2004
Cipate: 05-May-2000 #sequence_revision '05-May-2000 #text_change 09-Jul-2004
Cipate: 05-May-2000 #sequence_revision '05-May-2000 #text_change 09-Jul-2004
RiParkhill, J.; Achtman, M.; James, K.D.; Bentley, S.D.; Churcher, C.; Klee, S.R.; Morel
Nature 404, S02-506, 2000
A;Title: Complete DNA sequence of a serogroup A strain of Neisseria menigitidis Z2491.
A;Reference number: A81775; MUID:20222556; PMID:10761919
A;Status: preliminary

A;Molecule type: DNA A;Residues: 1-154 - cPAR. A;Cross-references: UNIPROT:Q9JTN1; GB:AL162756; GB:AL157959; NID:g7380091; PIDN:CAB8493 A;Experimental source: serogroup A, strain 22491

A,Gene: NMA1703 C,Superfamily: Escherichia coli ybdQ protein

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A)Cross-references: UNIPROT:P19785; GB:M38651; NID:g193119; PIDN:AAA37580.1; PID:g193180 c)Comment: The steroid hormones and their receptors are involved in the regulation of eul. C)Comment: In the absence of ligand, steroid hormone receptors are thought to be weakly & c)Comment: In the absence of ligand, steroid hormone receptors are thought to be weakly & c)Superfamily: estrogen receptor; erbA transforming protein homology c)Superfamily: estrogen receptor; erbA transforming protein homology c)Superfamily: estrogen receptor; phosphoprotein; steroid binding; steroid hormone recept F;1-137/Domain: amino-terminal <NH2> F;184-275/Domain: bNA binding #status predicted <DNA> F;187-460/Domain: erbA transforming protein homology <ERBA>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                exoskeletal protein HACP202B - American lobster (fragment)
C;Species: Homarus americanus (American lobster)
C;Date: 23-Jul-1997 #sequence_revision 01-Aug-1997 #text_change 09-Jul-2004
C;Date: 23-Jul-1997 #sequence_revision 01-Aug-1997 #text_change 09-Jul-2004
C;Accession: S77937
S;Nousiainen, M.; Rafn, K.; Skou, D.; Roepstorff, P.; Andersen, S.O.
Submitted to the Protein Sequence Database, June 1997
A;Description: Characterization of exoskeletal proteins from the American lobster, Homarn A;Reference number: S77925
A;Accession: S77935
A;Status: preliminary
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C;Species: Mus musculus (house mouse)
C;Date: 06-Mar-1992 #sequence_revision 14-Jul-1994 #text_change 09-Jul-2004
C;Accession: A40061
R;White, R.; Lees, J.A.; Needham, M.; Ham, J.; Parker, M.
Mol. Endocrinol. 1, 735-744, 1987
A;Title: Structural organization and expression of the mouse estrogen receptor.
A;Reference number: A40061; MUID:91042558; PMID:2484714
                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 189;
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Pred. No. 8;
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9 AAEKARFFQAFKAAEAAA 26
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A,Residues: 1-189 <NOU>
A,Cross-references: UNIPROT:Q7M495
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61.1%;
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Best Local Similarity
Matches 11; Conserv
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Matches 11, Conserv
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A; Residues: 1-599 <WHI>
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RESULT 5
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A;Cross-references: UNIPROT:Q8UBZ5; GB:AE008688; PIDN:AAL43684.1; PID:g17741210; GSPDB:G
A;Experimental source: strain C58 (Dupont)
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R;Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, I
R;Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Kutyavin, T.; Levy, R.; Li, M.; McClell
r; Karp, P.; Romero, P.; Zhang, S.
Science 294, 2317-2323, 2001
A;Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm,
                                                                                                                                                                                                                                                                                                                                                                                                           R;Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Qurollo, B.; Goldman, A.; Liu, F.; Wollam, C.; Allinger, M.; Doughty, D.; Scott, C.; Lappas, C.; Markelz, B.; Science 294, 2323-2328, 2001
A;Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium tum A;Reference number: A97359; MUID:21608551; PMID:11743194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A,Cross-references: UNIPROT:Q8UBZS; GB:AE007869; PIDN:AAK88423.1; PID:g15157917; GSPDB:Q
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                                                                                                                                                                                                                                                                                                        - Agrobacterium tumefaciens (strain C58, Cereon)
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A,Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.
A,Reference number: AB2577, MUID:21608550; PMID:11743193
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Length 154;
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A;Map position: circular chromosome
C;Superfamily: Escherichia coli ribosomal protein L19
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C,Superfamily: Escherichia coli ribosomal protein L19
Query Match 54.9%; Score 45; DB 2; Best Local Similarity 56.2%; Pred. No. 5.4; Matches 9; Conservative 4; Mismatches
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                                                                                                                                                                   48 APEFLOHESYEAAVA 63
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Matches 11; Conservative
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Residues: 1-179 <KUR>
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A;Status: preliminary
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Best Local Similarity 52.9
Matches 9; Conservative
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Best Local Similarity 62.5
Matches 10; Conservative
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A; Residues: 1-185 <HEI>
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A,Residues: 1-347 <PAR>
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A; Residues: 1-487, T., 489-600 cMAG>
A; Cross-references: EMBL:X61099; NID:956120; PIDN:CAA43411.1; PID:956121
C; Comment: The steroid hormones and their receptors are involved in the regulation of every c; Comment: In the absence of ligand, steroid hormone receptors are thought to be weakly omplex appears to recognize discrete DNA sequences upstream of transcriptional start sit C; Superfamily: estrogen receptor; erbA transforming protein homology
C; Ksywords: DNA binding; nucleus; phosphoprotein; steroid binding; steroid hormone receptor; respector; erbA transforming protein homology cRRBA>
F; 188-461/Domain: amino-terminal cMR2>
F; 188-461/Domain: anino-terminal cMR2>
F; 188-461/Domain: anino-terminal cMR3>
F; 188-461/Domain: are finger CCCC motif
F; 24-246/Region: zinc finger CCCC motif
F; 251-276/Region: nuclear location signal
F; 255//Domain: steroid binding site: zinc (Cys) #status predicted
F; 256, 232, 242, 245, Binding site: zinc (Cys) #status predicted
F; 226, 232, 242, 245, Binding site: zinc (Cys) #status predicted
F; 241, 310/Binding site: zinc (Cys) (Covalent) #status predicted
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C;Species: Mycobacterium tuberculosis
C;Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 09-Jul-2004
C;Accession: H70927
R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, Cole, S.T.; Bavies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S. Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.
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C;Species: Rattus norregicus (Norway rat)
C;Date: 30-Sep-1991 #sequence_revision 14-Jul-1994 #text_change 09-Jul-2004
C;Accession: S07379; S16731
R;Koike, S.; Sakai, M.; Muramatsu, M.
Nucleic Acids Res. 15, 2499-2513, 1987
A;Title: Molecular cloning and characterization of rat estrogen receptor CDN
A;Reference number: S07379; MUID:87174780; PMID:3031601
                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
F;187-210/Region: zinc finger CCCC motif
F;223-245/Region: zinc finger CCCC motif
F;260-275/Region: nuclear location aignal
F;304-556/Domain: steroid binding #status predicted <STB>
F;189,192,206,209/Binding site: zinc (Cys) #status predicted
F;225,231,241,244/Binding site: zinc (Cys) #status predicted
F;240,309/Binding site: phosphate (Ser) (covalent) #status predicted
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                                                                                                                                                                                                                                                       Score 44; DB 1; Length 599;
Pred. No. 30;
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Pred. No. 30;
0; Mismatches 5; Indels
                                                                                                                                                                                                                                 53.7%; Scc...
68.8%; Pred. No. 5c.,
... 0; Mismatches
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submitted to the EMBL Data Library, June 1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                53.7%;
68.8%;
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                                                                                                                                                                                                                                                                                                                                                                               2 PEKAKYEAYKAAAAA
                                                                                                                                                                                                                                                                                                                 11; Conservative
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Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Reference number: $16731
                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
Matches 11; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Molecule type: mRNA
A; Residues: 1-600 <KOI>
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T-cell receptor gamma chain precursor - sheep (fragment)
C;Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)
C;Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)
C;Date: 0.3-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 23-Jul-1999
C;Accession: 536290; 523041
R;Hein, W.R.; Dudler, L.
BEMBO J. 12, 715-724, 1993
A;Title: Divergent evolution of T cell repertoires: extensive diversity and developmenta A;Reference number: 536290; MUID:93178447; PMID:8440261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            probable rotamase NMA2206 [imported] - Neisseria meningitidis (strain Z2491 serogroup A) C;Species: Neisseria meningitidis C;Date: 05-May-2000 #sequence_revision 05-May-2000 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C;Accession: A81794
R;Parkhill, J.; Achtman, M.; James, K.D.; Bentley, S.D.; Churcher, C.; Klee, S.R.; Morel
R;Parkhill, J.; Achtman, M.; Jeather, S.; Moule, S.; Mungall, K.; Quail, M.A.; Rajandream, Nature 404, 502-506, 2000
A;Title: Complete DNA sequence of a serogroup A strain of Neisseria menigitidis Z2491.
A;Reference number: A81775; MUID:20222556; PMID:10761919
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Cross-references: UNIPROT:Q9JSP0; GB:AL162758; GB:AL157959; NID:g7380672; PIDN:CAB8541
A;Experimental source: serogroup A, strain 22491
                                                                                                                                                                                                                                          A;Cross-references: UNIPROT:Q10795; GB:Z74024; GB:AL123456; NID:g3250700; PIDN:CAA98346.
A;Experimental source: strain H37Rv
C;Genetics:
A, Authors: Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G. Syfitle: Deciphering the biology of Mycobacterium tuberculosis from the complete genome A; Reference number: A70500; MUID:98295987; PMID:9634230 A; Accession: H70927
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                                                                                                                            A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-162 <COL>
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C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: T-cell receptor
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62.5%; Pred. No. 25;
live 2; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                          43;
No.
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A;Reference number: S65398
A;Accession: S65398
A;Molecule type: mRNA
A;Molecule type: mRNA
A;Residues: 1-111, AIPEKKTL',120,'EEAK',125,'AQENA',131,'VEAEKKQEKTARTE',146,'EPTVEAQP',1
A;Cross-references: EMBL:X63828, NID:97663; PID:97664
A;Note: the differences in residues 112-178 are due to frameshift errors
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C;Species: Gallus gallus (chicken)
C;Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 16-Aug-2004
C;Accession: ISO145; S14512
Isoukemia 5, 357-360, 1991
A;Trile: CDNA cloning of a homeobox-containing gene expressed in avian myeloblastic virus
A;Reference number: ISO145; MUID:91238215; FMID:1674560
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C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                               C;Species: Drosophila melanogaster
C;Date: 01-Dec-1992 #sequence_revision 01-Dec-1992 #text_change 09-Jul-2004
                                                 Gaps
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C;Keywords: DNA binding; homeobox; nucleus; transcription regulation
F;96-152/Domain: homeobox homology <HOX>
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Pred. No. 32;
2; Mismatches 5; Indels
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R;Perkins, L.A.
submitted to the EMBL Data Library, December 1991
           Pred. No. 30;
0; Mismatches
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Pred. No. 20;
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A, Map position: 10
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                                                                                                                                                                                               215 AAEKAKAEAEKKAAA 229
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Best Local Similarity 58.8%;
Matches 10; Conservative
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       Similarity 73.3 11; Conservative
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Best Local Similarity
Matches 9; Conserv
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           Best Loca
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                                                                                                                                                                                                           peptidyl-prolyl, cis-trans isomerase NWB0281 [imported] - Neisseria meningitidis (strain C,Species: Neisseria meningitidis
C,Species: Neisseria meningitidis
C,Species: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 09-Jul-2004
C,Accession: B81216
R;Tettelin, H; Saunders, N.J; Heidelberg, J.; Jeffries, A.C; Nelson, K.E.; Eisen, J.A. Hickey, E.K.; Haft, D.H.; Salzberg, S.L.; White, O.; Fleischmann, R.D.; Dougherty, B.A.; in, H; Qin, H; Vamathevan, J.; Gill, J.; Scarlato, V.; Masignani, V.; Pizza, M. Science 287, 1809-1815, 2000
A;Authors: Grandi, G.; Sun, L.; Smith, H.O.; Fraser, C.M.; Moxon, E.R.; Rappuoli, R.; Ve A;Reference number: A81000; MUD:2017875; PMID:10710307
A;Accession: B81216
A;Accession: B81216
A;Accession: preliminary
A;Reference preliminary
A;Residues: 1-348 <TET>
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10/0657

told protein - Becherichia coli (strain K-12)

C;Species: Escherichia coli
C;Species: Bscherichia coli
C;Species: Bscherichia coli
C;Date: 07-5ep-1990 #sequence_revision 07-Sep-1990 #text_change 09-Jul-2004
C;Accession: JV0057; B64810
R;Levengood, S.K.; Webster, R.E.
A;Title: Nuclectide sequences of the tolA and tolB genes and localization of their produ A;Reference number: JV0057; MUID:90078104; PMID:2687247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Cross-references: UNIPROT:Q9K186; GB:AE002385; GB:AE002098; NID:g7225506; PIDN:AAF4073
A;Experimental source: serogroup B, strain MC58
C;Genetics:
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A;Residues: 1-421 <BLAT>
A;Cross-references: GB.XE000177; GB.U00096; NID:g1786955; PIDN:AAC73833.1; PID:g1786960;
A;Experimental source: strain K-12, substrain MG1655
C;Comment: tolA and tolB proteins are necessary for colicins E2, E3, A, and K to reach t
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A,Status: nucleic acid sequence not shown; translation not shown
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 348;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  F:14-34/Domain: transmembrane #status predicted <MSS>F:78-301/Domain: helical #status predicted <HSR>F:355-362/Region: nucleotide-binding motif A (P-loop)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 43; DB 2;
Pred. No. 25;
2; Mismatches
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||:||| : ||| || APQKAKTASAKAA 30
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APQKAKTASAKAAKAA 37
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 62.57
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A,Map position: 17 min
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A; Molecule type: DNA
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Query Match

Search completed: March 31, 2005, 02:42:28 Job time : 21.2903 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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OM protein - protein search, using sw model

March 31, 2005, 02:18:02 ; Search time 91.3065 Seconds (without alignments) 95.342 Million cell updates/sec Run on:

US-10-056-583A-88 82 1 APEKAKYEAYKAAAAA 17 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

1612378 seqs, 512079187 residues Searched:

1612378 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

UniProt_03:*
1: uniprot_sprot:*
2: uniprot_trembl:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description	296m46 homo sapien	Q64cp3 uncultured	Q9jtnl neisseria m	jyn4 neisseria m			Q75gc3 oryza sativ		Q9v7u6 drosophila	Q7m495 homarus ame	Q7m496 homarus ame	Q6lan9 rattus norv	Q8p7p0 xanthomonas	-		-	P19785 mus musculu	P06211 rattus norv	~	_	P66435 mycobacteri		P50887 drosophila	Q7s9p3 neurospora	Q9uan1 drosophila				Q9ng88 drosophila	_	29ng90 drosophila
SOFTERALES OF THE PARTY OF THE	Q96M46		O TNIL 60	Q9JYN4 Q9	GRTS	Q9VFL4 Q											ដ	, ESR1_RAT P(RS16_MYCTU P(RL22_DROME P		Q9UAN1 Q9						O69NGO
% Query Match Length DB	570 2	707 2	154 2	154 2	179 1	300 2	375 2	395 2	463 2	189 2	189 2	113 2	272 2	306 2	316 2	574 2	599 1	600 1	607 2	162 1	162 1	289 2	299 1	304 2	312 2	319 2	319 2	319 2	319 2	319 2	319 2
* Query Match	61.0	58.5	54.9	54.9	54.9	54.9	54.9	54.9	54.9	54.3	54.3	53.7	53.7	53.7	53.7	53.7	53.7	53.7	53.7	52.4	52.4	52.4	52.4	52.4	52.4	52.4	52.4	52.4	52.4	52.4	52.4
Score	50	48	45	45	45	45	45	45	45	44.5	44.5	44	44	44	44	44	44	44	44	43	43	43	43	43	43	43	43	43	43	43	43
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170
089J65 09JSP0 09K186 08K183 083KA1 08FAT 00COT 00COTS 00COTS 07CCF1 07SCZ8 07SCZ8
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33 33 34 34 34 44 44 44 44 44 44 44 44 4
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ALIGNMENTS

PRT; 570 AA. eated) st sequence update) st annotation update) Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.	PUBDEMENTALINGS OF THE PROPERTY OF THE PROPETTY OF THE PROPETT	ls 0; Gaps
PRT; 570 AA. reated) st sequence update) st annotation update) Craniata; Vertebrata; Eutele Catarrhini; Hominidae; Homo.	1285; H., Nagai K., Kimura K., Subbahara T., Tanaka K., Isono Y., Nakamura Y., Isono Y., Nakamura Y., Isono Y., Nakamura Y., Shibahara T., Tanakawa B., Sato K., Tanikawa M., Hiraoka S., Tohiba Y. S., Yosida M., Hotuta T., Hiraoka S., Tokaida M., Hotuta T., Shiohata N., Takami S., Terashima H., Tanigami A., Pujama A., Takami S., Terashima H., Tanigami A., Fujama A., Takami S., Terashima H., Tanigami A., Fujama A., Takami A., Takami S., Terashima J., Takami S., Terashima J., Takami S., Terashima J., Takami S., Takami A., Takami A., Takami A., Takami A., Takami A., Takami A., Fujama M., Tanigami A., Pujami Y., Takamashi Y., Kikuchi H., Masuho Y., Takamashi Y., Kikuchi H., Masuho Y., Kikuchi H., Masuho Y., Seberization of 21,243 futerization of 21,243 futerization of 21,243 futeres	3; Indels
; 570 AA. ed) sequence update) annotation update) uniata; Vertebrata;	K., Sug K., K., K., K., K., K., K., K., K., K.,	
570 AA.) quence up notation ata; Vert	whit I Nagai K Nagai N Nag	Mo. 1, matche
	ng1285; T., Otsuki T. T., Nagai K Y., Isono Y., nagi T., Wagai K Kodaira H., T., Furuya T., N., Saro K., M., Hiraoka H., A., Haraoka H., A., Haraoka H., a A., Sasaki c., Yosida H., a A., Sasaki c., Yosida H., a A., Haraoka H., Tani oyama A., Itah niro H., Tani oyama A., Itah niro H., Tani oyama A., Itah niro H., Tani oxaki K., Hira oxaki K., Hira oxaki K., Marana oxaki K., Marana oxaki K., Noria oxak	Fred. NO. 1/; 1; Mismatches
Tremblrel. 19, Cr. (Tremblrel. 19, La (Tremblrel. 19, La protein FLJ32830. (Human).	I=10.1038/n Nishikawa T Mi K., Sato Mi K., Sato Mi K., Kawai Y T., Iwayan Y., Kaku Y., K., Yokoi K., Yokoi Watanabe Shi T., Yam Watanabe Shi T., Yam Watanabe Shi H., Oshima N., Watanabe Shi T., Watanabe Shi T., Watanabe Shi T., Yam Mi T., Noguc Ima Y., Miz J., Noguc Ima Y., Miz J., Noguc Ima Y., Miz J., Noguc Ima Y., Miz J., Noguc J., Satoh T., J., Satoh T., J., Satoh T., J., Satoh T., J., Nomura J., J., Nomura J., J., Noguc J., Nog	., \$
INARY; Lrel. Lrel. Lrel. in FLJ in FLJ i, Chor	OI=10. Nishi Shi K., K K., K A., KAt. A., Wat. S., Wat. A., W A.,	at
PRELIMINARY; (TrEMBLrel. (TrEMBLrel. (TrEMBLrel. (TrEMBLrel. (Human). (Human). etazoa; Chor	OM N.A. 203; DOI=10.10 uki Y., Nishika ", Hayashi K., Saito K., Kaw Saito K., Katsu ihara K., Katsu inata M., Watan iguchi S., Wata iguchi	Similarity 59. 9; Conservative
1 96M46 96M46; 1-DEC-2001 1-DEC-2001 7POCHELICAL OWN SADIENS UKARYOCKA; M	International Control of the Complete of the	Matches 9; (
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Gaps

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STRAIN=MCS8 / Sergroup B;
MEDLINE=2015575; PubMed=10710307; DOI=10.1126/science.287.5459.1809;
Tettelin H., Saunders N.J., Heidelberg J.F., Jeffries A.C.,
Nelson K.E., Eisen J.A., Ketchum K.A., Hood D.W., Peden J.F.,
Dodson R.J., Nelson W.C., Gwinn M.L., DeBoy K.T., Peterson J.D.,
Hickey E.K., Haft D.H., Salberg S.L., White O., Fleischmann R.D.,
Dougherty B.A., Mason T.M., Ciecko A., Parksey D.S., Blair E.,
Citcon H., Clark B.B., Cotton M.D., Utterback T.R., Khouri H.M.,
Qin H., Vamathevan J.J., Gill J., Scarlato V., Masignani V., Pizza M.,
Grandi G., Sun L., Smith H.O., Fraser C.M., Moxon E.R., Rappuoli R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Complete genome sequence of Neisseria meningitidis serogroup B strain \mathsf{MCSB}^{\,\, \mathsf{L}}_{1,j}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Neisseria meningitidis (serogroup B).
Bacteria, Proteobacteria, Betaproteobacteria, Neisseriales,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          54.9%; Score 45; DB 2; Length 154; 56.2%; Pred. No. 30; ive 4; Mismatches 3; Indels
                                                                                                                                                                                                           Length 154;
                                                                                                                                                                                                                                                                          3; Indels
                                                                                                                   Complete proteome; Hypothetical protein.
SEQUENCE 154 AA; 16552 MW; C9C4AFDDF521D064 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pfam; PF00582; Usp; 1. PRINTS; PRO1438; UNRSLESTRESS. Complete proteome; Hypothetical protein. SEQUENCE 154 AA; 16524 MW; CBAB524DF5221CAB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-OCT-2000 (TrEMBLrel. 15, Last sequence update) 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
                                                                                                                                                                                                        54.9%; Score 45; DB 2; 56.2%; Pred. No. 30; ive 4; Mismatches
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(Rel. 41, Last sequence update)
(Rel. 45, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 154 AA.
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InterPro; IPR006015; Usp.
InterPro; IPR006016; UspA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-OCT-2000 (TrEMBLrel. 15, Created)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
                                                        Pfam; PF00582; Usp; 1.
PRINTS; PR01438; UNVRSLSTRESS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hypothetical protein NMB1500.
OrderedLocusNames=NMB1500;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; AE002499; AAF41856.1;
PIR; H81076; H81076.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Science 287:1809-1815(2000)
InterPro; IPR006015; Usp.
InterPro; IPR006016; UspA.
                                                                                                                                                                                                     Query Match
Best Local Similarity 56.23
Matches 9, Conservative
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Best Local Similarity 56.23
Matches 9; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HSSP; P44880; 1JMV.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=491;
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QBUBZS;
28-FEB-2003
28-FEB-2003
25-OCT-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 09JYN4;
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RL19_AGRT5
ID RL19_ACRT5
AC Q8UBZ5
DT 28-FEB
DT 28-FEB
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MEDLINE=2022556; PubMed=10761919; DOI=10.1038/35006655;
Parkhill J., Achtemn M., James K.D., Bentley S.D., Churcher C.M.,
Klee S.R., Morelli G., Beaham D., Brown D., Chillingworth T.,
Davies R.M., Davis P., Devlin K., Feltwell T., Hamlin N., Holroyd S.,
Jagels K., Leather S., Moule S., Mungall K.L., Quail M.A.,
Rajandream M.A., Rutherford K.M., Simmonds M., Skelton J.,
Whitchead S., Spratt B.G., Barrell B.G.,
"Complete DNA sequence of a serogroup A strain of Neisseria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hallam S.J., Purnam N., Preston C.M., Detter J.C., Rokhsar D., Richardson P.M., DeLong E.F., "Reverse methanogenesis: testing the hypothesis with environmental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Neisseria meningitidis (serogroup A).
Bacteria, Proteobacteria, Betaproteobacteria, Neisseriales,
Neisseriaceae, Neisseria.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              58.5%; Score 48; DB 2; Length 707; 70.6%; Pred. No. 43; 1.ve 1; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.

Putnam N., Detter J.C., Richardson P.M., Rokhsar D.;
Submitted (AUG-2004) to the EMBL/GenBank/DDBJ databases.
EMBL, XY714833; AAUS2834.1; -.

Hypothetical protein.
SEQUENCE 707 AA; 78670 MW; 104FE803EA51973D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
Hypothetical protein NMA1703.
OrderedLocusNames=NMA1703;
                                                                                                                                                                                                                                                                                                                                  Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                       707 AA.
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                                                                                                                                                                                                                                           PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Archaea, environmental samples.
NCBI_TaxID=286721;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 APEKAKYEAYKAAAAA 17
                                                                                                                                                                                                                                                                                                                                                                                                                       ORFNames=GZ1D1 21;
uncultured archaeon GZfos1D1
                                                                                                                                                                                                                                                                          (TrEMBLrel. 28,
                                                                                                                                                                                                                                                                                             25-OCT-2004 (TrEMBLrel. 28, 25-OCT-2004 (TrEMBLrel. 28, 25-OCT-2004 (TrEMBLrel. 28,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Science 305:1457-1462(2004).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Nature 404:502-506(2000).
EMBL; All62756; CAB84931.1;
PIR; BB1866; B81866
HSSP; P44880; IJMV.
                                                              ||| |||||
194 PEKVKYEAYRTLA 206
                            PEKAKYEAYKAAA 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity 70.6
Matches 12, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRELIMINARY;
                                                                                                                                                                                                                                       PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                              Hypothetical protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          meningitidis Z2491.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PubMed=15353801;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    genomics.
                            N
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                                                                                                                                                                                                                                                                    Q64CP3;
                                                                                                                                                                                                                                           Q64CP3
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RESULT 3 Q9JTN1

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Gaps

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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Agrobacterium tumefaciens C58.";
Science 294:2323-2328(2001).
-!- FUNCTION: This protein is located at the 30S-50S ribosomal subunit interface and may play a role in the structure and function of the aminoacyl-tRNA binding site (By similarity).
                                                                                                                                                               MEDLINE=21608550; PubMed=11743193; DOI=10.1126/science.1066804; MeDLINE=21608550; PubMed=11743193; DOI=10.1126/science.1066804; Mood D.W., Setubal J.C., Kaul R., Mond G.E., Almeida N.F. Jr., Woo L., Chan Y., Paulsen I.T., Bisen J.A., Karp P.D., Bovee D. Sr., Chapman P., Clendenning J., Deatherage G., Gillet W., Grant C., Kutyavin T., Levy R., Li M.-J., McClelland B., Palmieri A., Raymond C., Rouse G., Saenphimmachak C., Wu Z., Romero P., Gordon D., Zhang S., Yoo H., Tao Y., Biddle P., Jung M., Krespan W., Perry M., Gordon-Kamm B., Liao L., Kim S., Hendrick C., Zhao Z.-Y., Dolan M., Chumley R., Tingey S.V., Tomb J.-F., Gordon M.P., Olson M.V.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE-2166851; PubMed=11743194; DOI=10.1126/science.1066803; Goodner B., Hinkle G., Gattung S., Miller N., Blanchard M., Qurollo B., Goldman B.S., Cao Y., Askenazi M., Halling C., Mullin L., Houmiel K., Gordon J., Vaudin M., Iartchouk O., Epp A., Liu F., Wollam C., Allinger M., Doughty D., Scott C., Lappass C., Markelz B., Flanagan C., Crowell C., Gurson J., Lomo C., Sear C., Strub G., Cielo C., Slater S., "Genome sequence of the plant pathogen and biotechnology agent
                                                                                                                                                                                                                                                                                                                                                                                                                                  Nester E.W.; "The genome of the natural genetic engineer Agrobacterium tumefaciens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SIMILARITY: Belongs to the ribosomal protein 119P family.
50S ribosomal protein 119.

Name=rplS; OrderedLocusNames=Atu2703, AGR C 4900;
Agrobacterium tumefaciens (strain C58 / ATC 33970).
Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
Rhizobiaceae; Rhizobium/Agrobacterium group; Agrobacterium.
NCBI_TaxID=176299;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 54.9%; Score 45; DB 1; Length 179; Best Local Similarity 64.7%; Pred. No. 35; Matches 11; Conservative 1; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       179 AA; 19474 MW; F3256BA44A5AD2D1 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRINTS; PRO0061; RIBOSOWĀLLI9.
ProDom; PRO01979; Ribosomal Li9; 1.
TIGRPAMS; TIGR01024; rplS bact; 1.
PROSITE; PSO10105; RIBOSOWĀL Li9; 1.
Complete proteome; Ribosomal Li9; 1.
SEQUENCE 179 AA; 19474 MW. PROFEST.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HAMAP, MF 00402; -; 1.
InterPro; IPR001857; Ribosomal L19.
Pfam; PF01245; Ribosomal L19; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Science 294:2317-2323(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PIR, AF2908; AF2908.
PIR, F97683; F97683.
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REAUTINE-CROWN N.A.

WERDINTS-2019006; PubMed=10731132; DOI=10.1126/science.287.5461.2185; RADINTS-2019006; PubMed=10731132; DOI=10.1126/science.287.5461.2185; RADINTS-2019006; PubMed=10731132; DOI=10.1126/science.287.5461.2185; RADINTS-2019006; PubMed=10731132; DOI=10.1126/science.287.5461.2185; RADINTS-2019006; PubMed=10.7126; RADINTS-2019006; RADINTS-2019006; RADINTS-2019006; RADINTS-201906; 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
MEDLINE=22426070; PubMed=12537573;
Kaminker J.S., Bergman C.M., Kronmiller B., Carlson J., Svirskas R.,
Patel S., Frise E., Wheeler D.A., Lewis S.E., Rubin G.M.,
Ashburner M., Celniker S.E.;
"The transposable elements of the Drosophila melanogaster euchromatin:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=2146065; PubMed=12537568;
MEDLINE=22446065; PubMed=12537568;
MEDLINE=2146065; PubMed=12537568;
Celniker S.E., Wheeler D.A., Kronmiller B., Carlson J.W., Halpern A., Patel S., Adams M., Champe M., Dugan S.P., Frise E., Hodgson A., George R.A., Hoskins R.A., Laverty T., Muzny D.M., Nelson C.R., Patris B.D., Fichards S., Sodergren E.J., Svirskas R., Tabor P.E., Wan K., Stapleton M., Sutton G.G., Venter C., Weinstock G., Scherer S.E., Myers E.W., Gibbs R.A., Rubin G.M.; Finishing a Wold-genome shotgun: Release 3 of the Drosophila melanogaster euchromatic genome sequence.", Genome Biol. 3:RESEARCH0079-RESEARCH0079(2002).
                                                                                                                                                                                                                                                              Eukaryota, Metazoa, Arthropoda, Hexapoda, Insecta, Pterygota,
Neoptera, Endopterygota, Diptera, Brachycera, Muscomorpha,
Ephydroidea, Drosophilidae, Drosophila.
                                01-MAY-2000 (TrEMBLrel. 13, Created)
L-MAY-2000 (TrEMBLrel. 13, Last sequence update)
25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
CG14840-PA (AT18408p).
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                                                                                                                                                                                                                             Drosophila melanogaster (Fruit fly)
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                                                                                                                                                                                         ORFNames=CG14840;
                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=7227;
HILLER BERKER FREERER BERKER FREERER BERKER BERKER
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Gaps

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300 AA.

PRT;

PRELIMINARY;

O9VFL4 RESULT 6 Q9VFL4 ID Q9VFI

| |||: || | ||| | 135 AEEKARLEAEKVAAAQA 151 1 APEKAKYEAYKAAAAA 17

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05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Expressed protein, having alternative splicing products (Putative RNA pol II accessory factor) (With alternative splicing)
Name=08JNBb0031R14.2; SynonymasOSJNBB0034D21.3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                             MEDLINE-22456069; PubMed=12537572; Matthews B.B., Campbell K.S., Misra S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S., Hradecky P., Huang Y., Kaminker J.S., Millburn G.H., Prochnik S.E., Smith C.D., Tupy J.L., Whitfied E.J., Bayraktaroglu L., Berman B.P., Bettencourt B.R., Celniker S.E., de Grey A.D., Drysdale R.A., Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q., Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J., Champe M., Chavez C., Dorsett V., Dresnek D., Farfan D., Frise E., George R., Gonzalez M., Guarin H., Krommiller B., Li P., Liao G., Miranda A., Mungall C.J., Nunoo J., Pacleb J., Paragas V., Park S., Patel S., Phouanenavong S., Wan K., Yu C., Lewis S.E., Rubin G.M.,
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Bukaryota, Viridiplantes, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae;
Ehrhartoideae, Oryzeae, Oryza.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        Annotation of the Drosophila melanogaster euchromatic genome:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ;
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EMBL; AE003704; AAF55038.1; -.
EMBL; AY089356; AAL90094.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 to the EMBL/GenBank/DDBJ databases
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Submitted (MAR-2004) to the EMBL/GenBank/DDBJ databases
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SEQUENCE 300 AA; 31262 MW; 67D1586E3044A8FC CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Genome Biol. 3:RESEARCH0083-RESEARCH0083(2002).
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Pred. No. 57;
0; Mismatches
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InterPro; IPR007999; DUF745.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (SEP-2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  systematic review.";
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                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
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SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IntAct; Q9VFL4;
                                                                                                                                                                                                                                                                                                                                                                                                                                Lewis S.E.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                242
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10 56C3
10 055C3
AC 075G
AC 075G
DT 05-J
DT 0
RRYRRY RRYRY RRYRY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Erwinia carotovora (subsp. atroseptica) (Pectobacterium atrosepticum).
Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Pectobacterium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PubMed=15263089; DOI=10.1073/pnas.0402424101;
Bell K.S., Sebaihia M., Pritchard L., Holden M.T.G., Hyman L.J.,
Holeva M.C., Thomson N.R., Bentley S.D., Churcher L.J.C., Mungall K.,
Atkin R., Bason N., Brooks K., Chillingworth T., Clark K., Doggett J.,
Praser A., Hance Z., Hauser H.; Jagels K., Moule S., Norbertczak H.,
Ormond D., Price C., Quail M.A., Sanders M., Walker D., Whitehead S.,
Salmond G.P.C., Birch P.R.J., Parkhill J., Toth I.K.;
"Genome sequence of the enterobacterial phytopathogen Erwinia
                                                                                                                                                                                                                                                                                                 Gaps
                                                             Buell C.R., Yuan Q., Ouyang S., Liu J., Gansberger K., Jones K.M., Overton II L.L., Tsitrin T., Kim M.M., Bera J.J., Jin S.S., Fadrosh D.W., Tallon L.J., Koo H., Zismann V., Hsiao J., Blunt S., Vanaken S.S., Riedmuller S.B., Utterback T.T., Feldblyum T.V., Yang Q.Q., Haas B.J., Suh B.B., Peterson J.J., Quackenbush J., White O., Salzberg S.L., Fraser C.M.; Submitted (DEC-2002) to the EMBL/GenBank/DDBJ databases.

EMBL; AC145387; AAR88603.1; --
EMBL; AC145387; AAR88603.1; --
SEQUENCE 375 AA; 42035 MW; 3B060F30076D2264 CRC64;
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Buell R.;
Submitted (JAN-2004) to the EMBL/GenBank/DDBJ databases.
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25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            . Acad. Sci. U.S.A. 101:11105-11110(2004)
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Last annotation update)
                                                                                                                                                                                                                                                             DB 2;
70;
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                                                                                                                                                                                                                                                             54.9%; Score 45; 58.8%; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Tola protein.
Name=tola; OrderedLocusNames=ECA1372;
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178 APSSARHEPSSAAAAAA 194
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InterPro; IPR010528; TolA.
Pfam; PP06519; TolA; 1.
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01-OCT_2002 (TrEMBLrel. 22,
01-JUN-2003 (TrEMBLrel. 24,
                                                                                                                                                                                                                                                                             Best Local Similarity 58.8
Matches 10; Conservative
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Matches 12; Conservative
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                                                 SEQUENCE FROM N.A.
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Q6D7F3;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=22426065; PubMed=12537568;
Celniker S.E., Wheeler D.A., Kronmiller B., Carlson J.W., Halpern A., Patel S., Adams M., Champe M., Dugan S.P., Frise E., Hodgson A., George R.A., Hoskins R.A., Laverty T., Muzny D.M., Nelson C.R., Pacleb J.M., Park S., Pfeiffer B.D., Richards S., Sodergren E.J., Svirskas R., Tabor P.E., Wan K., Stapleton M., Sutton G.G., Venter C., Weinstock G., Scherer S.E., Myers E.W., Gibbs R.A., Rubin G.M.; "Finishing a Whole-genome shotgun: Release 3 of the Drosophila melanogaster euchromatic genome sequence.", Genome Biol. 3:RESEARCH0079-RESEARCH0079(2002).
                                                                                                                                                                                                                                                                 MEDLINE=20196006; PubMed=10731132; DOI=10.1126/science.287.5461.2185;
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Misra S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,
                                    Drosophila melanogaster (Fruit fly).

Bukaryota, Metazoa, Arthropoda, Hexapoda, Insecta, Pterygota,
Neoptera, Endopterygota, Diptera, Brachycera, Muscomorpha,
Ephydroidea, Drosophilidae, Drosophila.
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MEDLINE=22426070; PubMed=12537573;
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Hradecky P., Huang Y., Kaminker J.S., Millburn G.H., Prochnik S.E., Smith C.D., Tupy J.L., Whitfied E.J., Bayraktarcglu L., Berman B.P., Bettencourt B.R., Celniker S.E., de Grey A.D., Drysdale R.A., Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q., Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
                                                                                                           Lewis S.E.; annotation of the Drosophila melanogaster euchromatic genome:
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Submitted (JUN-1997) to the PIR data bank.
PIR; S77935; S77935.
NON_TER 1
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Nephropoidea, Nephropidae, Homarus.
NCBI_TaxID=6706,
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                                                                                                                                                                                                                                                           Submitted (SEP-2002) to the EMBL/GenBank/DDBJ databases
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SEQUENCE 463 AA; 49366 MW; 8D35569BEFBGEBC9 CRC64;
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01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Exoskeletal protein HACP202B (Fragment).
Homarus americanus (American lobster).
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01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
11-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Exoskeletal protein HACP202A (Fragment).
Homarus americanus (American lobster).
                                                                                                                                                                       Genome Biol. 3:RESEARCH0083-RESEARCH0083(2002).
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86;
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Pred. No. 44;
4; Mismatches
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| AAEKARFFQAFKAAEAAA 26
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InterPro; IPR007999; DUF745.
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Best Local Similarity 61.1:
Matches 11; Conservative
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01-MAR-2004
                                                                                                                                                     systematic
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SEQUENCE
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25-OCT-2004 (TrEMBLrel. 28, Created)
25-OCT-2004 (TrEMBLrel. 28, Last seq
25-OCT-2004 (TrEMBLrel. 28, Last ann
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EMBL, AE012368; AAM41843.1; -.

EO, GO:0005524; F.ATP binding; IEA.

InterPro; IPR000808; Mrp.

PROSITE; PS01215; MRP; 1.
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        Kanthomonadaceae; Xanthomonas
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SEQUENCE 272 AA
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                               NCBI_TaxID=340;
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25-0CT-2004
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ID 0
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                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GO; GO:0005634; C:nucleus; IEA.
GO; GO:0003677; F:DNA binding; IEA.
GO; GO:0004872; F:receptor activity; IEA.
GO; GO:0005496; F:steroid binding; IEA.
GO; GO:0003707; F:steroid hormone receptor activity; IEA.
GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
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Bacteria; Proteobacteria; Gammaproteobacteria; Xanthomonadales;
                                                                                                                           Nousiainen M., Rafn K., Skou L., Roepstorff P., Andersen S.O.; Submitted (JUN-1997) to the PIR data bank.

PIR, 877930; 877930.

NON_TER 18 189

SEQUENCE 189 AA; 20154 MW; 72A4EFCD9C647FE9 CRC64;
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                                                                                                                                                                                                                                                                                   DB 2; Length 189;
                 Eumalacostraca; Bucarida; Decapoda; Pleocyemata; Astacidea;
Nephropoidea; Nephropidae; Homarus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   53.7%; Score 44; DB 2; Length 113; 68.8%; Pred. No. 32; ive 0; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                           2; Indels
Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN=Sprague-Dawley;
Freyeschius B., Grandien K.;
Submitted (UN-1996) to the EMBL/GenBank/DDBJ databases.
EMBL; X98216; CAA66888.1; -.
                                                                                                                                                                                                                                         72A4EFCD9C647FE9 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      113 113 113 1151 MW; A820B1196B918387 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Hypothetical protein NCC2571.
OrderedLocusNames=XCC2571;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              272 AA.
                                                                                                                                                                                                                                                                                 Score 44.5; DE Pred. No. 44; 4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            113 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Estrogen receptor protein (Fragment)
Rattus norvegicus (Rat).
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                                                                                                                                                                                                                                                                                                                                                                                            9 AAEKARFFQAFKAAEAAA 26
                                                                                                                                                                                                                                                                                                                                                                    1 APEKAK-YEAYKAAAAA 17
                                                                                                                                                                                                                    189 189
189 AA; 20154 MW;
                                                                                                                                                                                                                                                                                   54.3%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PEGAAYEFNAAAAAA 70
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01-OCT-2002 (TrEMBLrel. 22,
01-OCT-2003 (TrEMBLrel. 25,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pfam; PF02159; Oest recep; 1
PRINTS; PR00543; OESTROGENR
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Best Local Similarity
Local Similarity
Local 11; Conservative
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les 11; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=10116;
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Best Local Si
Matches 11;
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                                                                                                           SEQUENCE
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Q8P7P0;
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066LAN9
AC Q6LAN0
DT 05-JU
DT
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COBPTPO
10 COBPTP
AC COBPTP
DT 01-OC
DT 01-OC
DT 01-OC
DT 01-OC
DT OT
COC
DE HYDEL
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SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

SEQUENCE STRAIN=ATCC 33913 / NCPPB 528;

WEDIINE=22022145; bubMed=12024217; DOI=10.1038/417459a;

WEDIINE=22022145; bubMed=12024217; DOI=10.1038/417459a;

A silva A.C.R., Ferro J.A., Reinach F.C., Farah C.S., Furlan L.R.,

Quaggio R.B., Monteiro-Vitorello C.B., Van Sluys M.A., Almeida N.F.,

Alves L.M.C., do Amaral A.M., Bertolini M.C., Camargo L.B.A.,

Alves L.M.C., do Amaral A.M., Bertolini M.C., Camargo L.B.A.,

Alves L.M.C., do Amaral A.M., Sertolini M.C., Cramargo L.B.A.,

Raria J.B., Ferreira A.J.S., Ferreira R.C.C., Ferro M.I.T.,

Paria J.B., Ferreira A.J.S., Ferreira R.C.C., Gruber A.,

Ratsuyama A.M., Kishi L.T., Leite R.P., Lemos B.G.M., Lemos M.Y.F.,

Locali E.C., Machado M.A., Madeira A.M.B.N., Martine Z.R.O. Meidanis J.M., Menck C.F. M., Moron D.H.,

Moreira L.M., Novo M.T.M., Okura V.R., Oliveira M.C., Oliveira V.R.,

Spinola L.A.F., Takita M.A., Tamura R.E., Teixeira B.C., Tezza R.I.D.,

Spinola L.A.F., Takita M.A., Tamura R.E., Teixeira B.C., Tezza R.I.D.,

Trindade dos Santos M., Truffi D., Tsai S.M., White F.F.,

Retubal J.C., Katajima J.P.,

"Comparison of the genomes of two Xanthomonas pathogens with differing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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Oryza sativa (japonica cultivar-group).
Eukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
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"Oryza sativa nipponbare(GA3) genomic DNA, chromosome 7, PAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
Hypothetical protein OSJNBa0072106.16 (Hypothetical protein P049306.31).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 53.7%; Score 44; DB 2; Length 272; Best Local Similarity 66.7%; Pred. No. 75; Matches 10; Conservative 1; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
Sasaki T., Matsumoto T., Katayose Y.;
Sasaki T., Matsumoto T., Katayose Y.;
"Oryza sativa niponbare(GA3) genomic DNA, chromosome 7, 1 clone:OSJNBa0072106.";
Submitted (MAY-2003) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  clone:P0493C06.";
Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.
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EMBL; AP005193; BAD31146.1; -.
GO; GO:0046872; F:metal ion binding; IEA.
GO; GO:0030001; F:metal ion transport; IEA.
InterPro; IPR006121; HeavyMe_transpt.
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306 AA; 32378 MW; A60288C9B77E8868 CRC64;

SEQUENCE

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STRAIN=VPI-5482 / ATCC 29148;
STRAIN=VPI-5482 / ATCC 29148;
MEDLINE=225508088; Pubmed=12663928; DOI=10.1126/science.1080029;
Xu J., Bjursell M.K., Himrod J., Deng S., Carmichael L.K.,
Chiang H.C., Hooper L.V., Gordon J.I.;
A genomic view of the human-Bacteroides thetaiotaomicron symbiosis.";
Science 299:2074-2076(2003).
EMBL; AE0166930; AA076233.1; ...
InterPro; IPR005094; Relaxase.
Pffam; PF03422; Relaxase.
Complete proteome.
SEQUENCE 316 AA; 36130 MW; B63E149ACEDEC898 CRC64;
                                                                                                    Gaps
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Query Match 53.7%; Score 44; DB 2; Length 306; Best Local Similarity 68.8%; Pred. No. 84; Matches 11; Conservative 1; Mismatches 4; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Order-1003 (TrEMBLrel. 24, Created)
01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
Mobilization protein BmgA.
OrderedLocusNames=BT1126;
Bacteroides thetalotaomicron.
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122 PEKEAAKADKAAAAA 137
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Best Local Similarity 56.2
Matches 9; Conservative
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01-JUN-2003
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08A8P1
AC 08A8P
AC 08A8P
DT 01-JU
DT 01-JU
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Search completed: March 31, 2005, 02:41:09 Job time : 93.3065 secs

171 ASEKVKYEIYRAVKEA 186

1 APEKAKYEAYKAAAAA 16

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Abp52304 HIA-DR2 m
Abp52303 HIA-DR2 m
Abp52299 HIA-DR2 m
Abp52290 HIA-DR2 m
Abp52300 HIA-DR2 m
Abp52209 HIA-DR2 m
Abp52299 HIA-DR2 m
Abp52299 HIA-DR2 m
Abp52291 HIA-DR2 m
Abp52293 HIA-DR2 m
Abp65293 HIA-DR2 m
Adp60395 B. lichen
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HLA-DR2 m
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Drosophil
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65.338 Million cell updates/sec
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                                              March 31, 2005, 02:17:12; Search time 88.7903 Seconds
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5.1.6
Compugen Ltd.
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                                                                                                                                     2105692 seqs, 386760381 residues
GenCore version
Copyright (c) 1993 - 2005
                                                                                                                                                                                                              first 45 summaries
                              protein search, using sw model
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ABP52305
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ABP52289
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ABP52294
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ABP52295
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ADN60395
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ABP52302
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Gapop 10.0 , Gapext 0.5
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geneseqp1990s:*
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geneseqp2001s:*
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length: 2000000000
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76
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Maximum Match
Listing first
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Match 1
                                                                                                                                                                                                                                                                                                                                                                                                                      seq
seq
                                                                                      Perfect score:
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                               1
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Ads96704 Drosophil Abp52264 HLA-DR2 m			Abp52257 HLA-DR2 m	Abu23345 Protein e	Abp52265 HLA-DR2 m	Abp79775 N. gonorr		Abu37170 Protein e	Adp08309 Neisseria	Abb59072 Drosophil	Abp52254 HLA-DR2 m	Abp52255 HLA-DR2 m	Abp52240 HLA-DR2 m	Abp52253 HLA-DR2 m	Abp52251 HLA-DR2 m	Abp52241 HLA-DR2 m	Abp52249 HLA-DR2 m	Abp52239 HLA-DR2 m
ADS96704 ABP52264	ABP52267	ABP52259	ABP52257	ABU23345	ABP52265	ABP79775	ABU38057	ABU37170	ADP08309	ABB59072	ABP52254	ABP52255	ABP52240	ABP52253	ABP52251	ABP52241	ABP52249	ABP52239
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59	59	50	50	57	26	99	26	26	26	26	55	25	22	55	55	55	55	55
46 45	45	45	45	44	43	43	43	43	43	43	42	42	42	42	42	42	42	42
26	28	53	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

Human leukocyte antigen; HLA; major histocompatibility complex; MHC; HLA-DR2; MHC class II DR-2 molecule; demyelinating; multiple sclerosis; immune response; antiinflammatory; neuroprotective; proliferation; MHC class II protein inhibitor; demyelinating disease; inhibition; post-viral encephalomyelitis; post-vaccine demyelinating condition; HLA-DR2 molecule binding peptide SEQ ID NO:91. ABP52297 standard; peptide; 15 AA anti-tumour necrosis factor agent 24-JAN-2002; 2002WO-US002071. 24-JAN-2001; 2001US-0263569P (first entry) WO200259143-A2. sapiens 16-OCT-2002 01-AUG-2002 Synthetic. ABP52297;

(HARD) HARVARD COLLEGE

Strominger JL, Fridkis-Hareli

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WPI; 2002-608439/65.

æ a major treating New compositions comprising synthetic peptides in complex with histocompatibility complex class II HLADR2 protein, useful for demyelinating disease, e.g. multiple sclerosis, or post-viral encephalomyelitis.

Claim 28; Page 39; 54pp; English.

The present invention describes compositions (I) comprising a peptide with an amino acid sequence with tyrosine (Y), lysine (K), and/or valine residues. The complex of the peptide with a major histocompatibility complex (MHC) class II HLA-DR2 protein is involved in modulating an immune response. (I) has antiinflammatory and neuroprotective activities, and can be used as a MHC class II protein inhibitor. The compositions comprising the peptides are useful for treating demyelinating diseases

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Gaps

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Length 15; 0: Indels

Score 73; DB 5; 1 Pred. No. 4.3e-05; 1; Mismatches 0

1;

15

1 EKPKFEAYKAAAPA Conservative

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96.1%; 93.3%;

Similarity

Query Match Local

14;

Matches

Sequence 15 AA;

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such as multiple sclerosis, post-viral encephalomyelitis, a post-vaccine demyelinating condition, and a side effect of administering an antitumour necrosis factor agents. The peptide further inhibits proliferation of autoantigen-specific HiA-DR2-restricted T cell clones. ABP52207 to ABP52305 represent peptides used in the exemplification of the present
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                                                                                                                                                                                                                                                                                                     Local Similarity
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Synthetic.
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The present invention describes compositions (I) comprising a peptide with an amino acid sequence with tyrosine (Y), lysine (K), and/or valine residues. The complex of the peptide with a major histocompatibility complex (MHC) class II HLA-DR2 protein is involved in modulating an immune response. (I) has antiinflammatory and neuroprotective activities, and can be used as a MHC class II protein inhibitor. The compositions such as multiple sclerosis for treating demyelinating diseases such as multiple sclerosis, post-viral encephalomyelitis, a post-vaccine demyelinating condition, and a side effect of administering an antitumour necrosis factor agents. The peptide further inhibits proliferation of autoantigen-specific HLA-DR2-restricted T cell clones. ABP52207 to ABP52305 represent peptides used in the exemplification of the present
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New compositions comprising synthetic peptides in complex with a major histocompatibility complex class II HLADR2 protein, useful for treating a demyelinating disease, e.g. multiple sclerosis, or post-viral encephalomyelitis.
                                                                                                                                                                                                                                                                                                                                          Human leukocyte antigen; HLA; major histocompatibility complex; MHC; HLA-DR2; MHC class II DR-2 molecule; demyelinating; multiple sclerosis; immune response; antiinflammatory; neuroprotective; proliferation; MHC class II protein inhibitor; demyelinating disease; inhibition; post-viral encephalomyelitis; post-vaccine demyelinating condition;
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Pred. No. 0.00013;
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(first entry)
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Best Local Similarity 93.33
Matches 14; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human leukocyte antigen; HLA; major histocompatibility complex; MHC; HLA-DR2; MHC class II DR-2 molecule; demyelinating; multiple sclerosis; immune response; antiinflammatory; neuroprotective; proliferation; MHC class II protein inhibitror; demyelinating disease; inhibition; post-viral encephalomyelitis; post-vaccine demyelinating condition; anti-tumour necrosis factor agent.
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                                                100.0%; Score 76; DB 5; Length 15; 100.0%; Pred. No. 1.4e-05; ive 0; Mismatches 0; Indels
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Gaps

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with an amino acid sequence with tyrosine (Y), lysine (K), and/or valine residues. The complex of the peptide with a major histocompatibility complex (MHC) class II HLA-DR2 protein is involved in modulating an immune response. (I) has antiinflammatory and neuroprotective activities, and can be used as a MHC class II protein inhibitor. The compositions comprising the peptides are useful for treating demyelinating diseases such as multiple sclerosis, post-viral encephalomyelitis, a post-vaccine demyelinating condition, and a side effect of administering an anti-tumour necrosis factor agents. The peptide further inhibits proliferation of autoantigen-specific HLA-DR2-restricted T cell clones. ABB52307 to
                                                                                                                                                                                                                                       Human leukocyte antigen; HLA; major histocompatibility complex; MHC; HLA-DR2; MHC class II DR-2 molecule; demyelinating; multiple sclerosis; immune response; attiinflammacory; neuroprotective; proliferation; MHC class II protein inhibitor; demyelinating disease; inhibition; post-viral encephalomyelitis; post-vaccine demyelinating condition; anti-tumour necrosis factor agent.
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Pred. No. 0.0002;
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                                                                                                                                                                                                      HLA-DR2 molecule binding peptide SEQ ID NO:93.
                                                                                                      ABP52299 standard; peptide; 15 AA.
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93.3%;
EKPKFEAYKAAAAPA 15
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                                                                                                                                                                       (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New compositions comprising synthetic peptides in complex with a major histocompatibility complex class II HLADR2 protein, useful for treating demyelinating disease, e.g. multiple sclerosis, or post-viral encephalomyelitis.
                                                                                                           Human leukocyte antigen; HLA; major histocompatibility complex; MHC; HLA-DR2; MHC class II DR-2 molecule; demyelinating; multiple sclerosis; immune response; antiinflammatory; neuroprotective; proliferation; MHC class II protein inhibitor; demyelinating disease; inhibition; post-viral encephalomyelitis; post-vaccine demyelinating condition;
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Pred. No. 0.00033;
0; Mismatches 1; Indels
                                                                            HLA-DR2 molecule binding peptide SEQ ID NO:97.
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                                                                                                                                                                                               anti-tumour necrosis factor agent
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                                               16-OCT-2002 (first entry)
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                  ABP52303;
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Best Local 9
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ABP52303 standard; peptide; 17 AA.

RESULT 5 ABP52303 ID ABP5

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The present invention describes compositions (1) comprising a peptide with an amino acid sequence with tyrosine (Y), lysine (R), and/or value residues. The complex of the peptide with a major histocompatibility complex (WHC) class II HLA-DR2 protein is involved in modulating an immune response. (I) has antiinflammatory and neuroprotective activities, and can be used as MHC class II protein inhibitor. The compositions comprising the peptides are useful for treating demyelinating diseases such as multiple sclerosis, post-viral encephalomyelitis, a post-vaccine demyelinating condition, and a side effect of administering an antitumour necrosis factor agents. The peptide further inhibits proliferation of autoantigen-specific HLA-DR2-restricted T cell clones ABP52207 to
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Human leukocyte antigen; HLA; major histocompatibility complex; MHC; HLA-DR2; MHC class II DR-2 molecule; demyelinating; multiple sclerosis; immune response; antiinflammatory; neuroprotective; proliferation; MHC class II protein inhibitror; demyelinating disease; inhibition; post-viral encephalomyelitis; post-vaccine demyelinating condition; anti-tumour necrosis factor agent.
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                              Gaps
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0
Score 67; DB 5; Length 15;
Pred. No. 0.00042;
1; Mismatches 1; Indels
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HLA-DR2 molecule binding peptide SEQ ID NO:86.
                                  ABP52292 standard; peptide; 15 AA.
| ||:|||||||||||||
EAPKYEAYKAAAAPA 15
                                                         16-OCT-2002 (first entry)
                     원
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Human leukocyte antigen; HLA; major histocompatibility complex; MHC; HLA-DR2; MHC class II DR-2 molecule; demyelinating; multiple sclerosis; immune response; antiinflammatory; neuroprotective; proliferation; MHC class II protein inhibitor; demyelinating disease; inhibition; post-viral encephalomyelitis; post-vaccine demyelinating condition; anti-tumour necrosis factor agent.

HLA-DR2 molecule binding peptide SEQ ID NO:96,

16-OCT-2002 (first entry)

ABP52302 standard; peptide; 17 AA.

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Human leukocyte antigen, HLA; major histocompatibility complex, MHC; HLA-DR2; MHC class II DR-2 molecule; demyelinating; multiple sclerosis; immune response; antihiflammatory; neuroprotective; proliferation; MHC class II protein inhibitor; demyelinating disease; inhibition; post-viral encephalomyelitis; post-vaccine demyelinating condition; anti-tumour necrosis factor agent.
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WO200259143-A2

01-AUG-2002

sapiens

Homo

Synthetic

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The present invention describes compositions (I) comprising a peptide with an amino acid sequence with tyrosine (Y), lysine (K), and/or valine residues. The complex of the peptide with a major histocompatibility complex (MHC) class II HLA-DR2 protein is involved in modulating an immune response. (I) has antiinflammatory and neuroprotective activities, and can be used as a MHC class II protein inhibitor. The compositions comprising the peptides are useful for treating demyelinating diseases such as multiple sclerosis, post-viral encephalomyelitis, a post-vaccine demyelinating condition, and a side effect of administering an anti-tumour necrosis factor agents. The peptide further inhibits proliferation of autoantigen-specific HLA-DR2-restricted T cell clones. ABP52207 to
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New compositions comprising synthetic peptides in complex with a major histocompatibility complex class II HLADR2 protein, useful for treating demyelinating disease, e.g. multiple sclerosis, or post-viral
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                                                                                                                            encephalomyelitis.
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Fridkis-Hareli

Strominger JL,

WPI; 2002-608439/65

(HARD) HARVARD COLLEGE

24-JAN-2002; 2002WO-US002071. 24-JAN-2001; 2001US-0263569P.

WO200259143-A2

Synthetic.

01-AUG-2002

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The present invention describes compositions (I) comprising a peptide with an amino acid sequence with tyrosine (Y), lysine (K), and/or value residues. The complex of the peptide with a major histocompatibility complex (MHC) class II HIA-DR2 protein is involved in modulating an immune response. (I) has antiinflammatory and neuroprotective activities, and can be used as a MHC class II protein inhibitor. The compositions comprising the peptides are useful for treating demyelinating diseases such as multiple sclerosis, post-viral encephalomyelitis, a post-vaccine demyelinating condition, and a side effect of administering an antitumour necrosis factor agents. The peptide further inhibits proliferation of autoantigen-specific HIA-DR2-restricted T cell clones. ABP52207 to ABP52305 represent peptides used in the exemplification of the present
                                                         New compositions comprising synthetic peptides in complex with a major histocompatibility complex class II HLADR2 protein, useful for treating a demyelinating disease, e.g. multiple sclerosis, or post-viral encephalomyelitis.
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Pred. No. 0.0019;
.; Mismatches 1; Indele
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HLA-DR2 molecule binding peptide SEQ ID NO:99.
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                                                                                                                                                                                             Claim 28; Page 39; 54pp; English.
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86.7%;
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EKPKEEAFKAAAPA 15
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                        WPI; 2002-608439/65.
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Best Local Similarity
Matches 13; Conserv
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                                                                                                                                                                                                                                       New compositions comprising synthetic peptides in complex with a major histocompatibility complex class II HLADR2 protein, useful for treating demyelinating disease, e.g. multiple sclerosis, or post-viral
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                                                                                                                                           Strominger JL, Fridkis-Hareli M;
                                                                                                                                                                                                                                                                                                                                                            Claim 28; Page 39; 54pp; English.
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24-JAN-2002; 2002WO-US002071
                                                 24-JAN-2001; 2001US-0263569P.
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86.7%;
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EKAKFEAFKAAAAPA 17
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                                                                                            (HARD ) HARVARD COLLEGE
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Best Local Similarity
Matches 13; Conserv
                                                                                                                                                                                                                                                                                                               encephalomyelitis.
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invention

Synthetic

Homo

ABP52300;

RESULT 9 ABP52300

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Gaps ; 0

Claim 28; Page 39; 54pp; English

The present invention describes compositions (1) comprising a peptide with an amino acid sequence with tyrosine (Y), lysine (K), and/or valine residues. The complex of the peptide with a major histocompatibility complex (WHC) class II HLA-DS protein is involved in modulating an immune response. (I) has antiinflammatory and neuroprotective activities, and can be used as MHC class II protein inhibitor. The compositions comprising the peptides are useful for treating demyelinating diseases such as multiple sclerosis, post-viral encephalomyelitis, a post-vaccine demyelinating condition, and a side effect of administering an antituour necrosis factor agents. The peptide further inhibits proliferation of autoantigen-specific HLA-DS2-restricted T cell clones. ABBF52307 to ABPF53305 represent peptides used in the exemplification of the present invention

Sequence 15 AA;

Length 15; Score 63; DB 5; Length 15; Pred. No. 0.0019; 0; Mismatches 2; Indels 82.9%; 1 EKPKFEAYKAAAAPA 15 1 EAPKVEAYKAAAAPA 15 Local Similarity 86.7 1es 13; Conservative Query Match Best Loca Matches ò 셤

ABP52271 standard; peptide; 15 AA.

ABP52271;

(first entry) 16-OCT-2002

HLA-DR2 molecule binding peptide SEQ ID NO:65

Human leukocyte antigen; HLA; major histocompatibility complex; MHC; HLA-DR2; MHC class II DR-2 molecule; demyelinating; multiple sclerosis; immune response; antiinflammatory; neuroprotective; proliferation; MHC class II protein inhibitor; demyelinating disease; inhibition; post-viral encephalomyelitis; post-vaccine demyelinating condition; anti-tumour necrosis factor agent.

sapiens.

Synthetic

WO200259143-A2.

01-AUG-2002.

24-JAN-2002; 2002WO-US002071

24-JAN-2001; 2001US-0263569P

(HARD) HARVARD COLLEGE

Fridkis-Hareli M; Strominger JL,

WPI; 2002-608439/65.

New compositions comprising synthetic peptides in complex with a major histocompatibility complex class II HLADR2 protein, useful for treating a demyelinating disease, e.g. multiple sclerosis, or post-viral encephalomyelitis.

Claim 28; Page 39; 54pp; English.

The present invention describes compositions (I) comprising a peptide with an amino acid sequence with tyrosine (Y), lysine (K), and/or valine residues. The complex of the peptide with a major histocompatibility complex (MHC) class II HLA-DR2 protein is involved in modulating an

immune response. (I) has antiinflammatory and neuroprotective activities, and can be used as AMC class II protein inhibitor. The compositions comprising the peptides are useful for treating demyelinating diseases such as multiple sclerosis, post-viral encephalomyelitis, a post-vaccine demyelinating condition, and a side effect of administering an anti-umour necrosis factor agents. The peptide further inhibits proliferation of autoantigen-specific HIA-NBZ-restricted T cell clones, ABB52207 to ABB52305 represent peptides used in the exemplification of the present invention

Sequence 15 AA; 8555555555558

Gaps ö Score 57; DB 5; Length 15; Pred. No. 0.019; 2; Indels 1; Mismatches 75.0%; 80.08; Watches 12; Conservative Query Match

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RESULT 12

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Gaps ; 0

ABP52289 standard; peptide; 15 AA. ABP52289

ABP52289;

(first entry) 16-OCT-2002 HLA-DR2 molecule binding peptide SEQ ID NO:83.

Human leukocyte antigen; HLA; major histocompatibility complex; MHC; HLA-DR2; MHC class II DR-2 molecule; demyelinating; multiple sclerosis; immune response; antiinflammacory; neuroprotective; proliferation; MHC class II protein inhibitor; demyelinating disease; inhibition; post-viral encephalomyelitis; post-vaccine demyelinating condition; anti-tumour necrosis factor agent.

sapiens. Homo

Synthetic

WO200259143-A2.

01-AUG-2002

24-JAN-2002; 2002WO-US002071.

24-JAN-2001; 2001US-0263569P.

HARD) HARVARD COLLEGE

Fridkis-Hareli Strominger JL,

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WPI; 2002-608439/65

New compositions comprising synthetic peptides in complex with a major histocompatibility complex class II HLADR2 protein, useful for treating demyelinating disease, e.g. multiple sclerosis, or post-viral

encephalomyelitis.

Claim 28; Page 39; 54pp; English.

The present invention describes compositions (I) comprising a peptide with an amino acid sequence with tyrosine (Y), lysine (K), and/or valine residues. The complex of the peptide with a major histocompatibility complex (MHC) class II HLA-DR2 protein is involved in modulating an immune response. (I) has antiinflammatory and neuroprotective activities, and can be used as a MHC class II protein inhibitor. The compositions comprising the peptides are useful for treating demyelinating diseases such as multiple sclerosis, post-viral encephalomyelitis, a post-vaccine demyelinating condition, and a side effect of administering an anti-tumour necrosis factor agents. The peptide further inhibits proliferation of autoantigen-specific HLA-DR2-restricted T cell clones. ABP52207 to

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Matches

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ABP52305 represent peptides used in the exemplification of the present
                                                                                                                                             Gaps
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                                                                                                  Length 15;
                                                                                                                                         2; Indels
                                                                                                  Score 57; DB 5;
Pred. No. 0.019;
2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                       HLA-DR2 molecule binding peptide SEQ ID NO:92.
                                                                                                                                                                                                                                                                                                                               ABP52298 standard; peptide; 15 AA.
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                                                                                                Query Match
Best Local Similarity
Matches 11; Conserv
                                                            Sequence 15 AA;
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                       invention
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Score 57; DB 5; Length 15; Pred. No. 0.019;

75.0**%**; 80.0**%**;

Best Local Similarity

Query Match

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New compositions comprising synthetic peptides in complex with a major histocompatibility complex class II HLADR2 protein, useful for treating a demyelinating disease, e.g. multiple sclerosis, or post-viral encephalomyelitis.
                                                                                                                                                                                                                                                                          HIA-DR2; MHC class II DR-2 molecule, demyelinating; multiple sclerosis; limmune response; antiinflammatory; neuroprotective; proliferation; MHC class II protein inhibitor; demyelinating disease; inhibition; post-viral encephalomyelitis; post-vaccine demyelinating condition; anti-tumour necrosis factor agent.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          present invention describes compositions (I) comprising a peptide
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                                                                                                                                                                                                                                                              Human leukocyte antigen; HLA; major histocompatibility complex; MHC;
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                                                                                                                                                                                                                         HLA-DR2 molecule binding peptide SEQ ID NO:88.
                                                                                                                    ABP52294 standard; peptide; 17 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Fridkis-Hareli M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 28; Page 39; 54pp; English.
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                                1 EKAKYEAYKAAAAA
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The present invention describes compositions (I) comprising a peptide with an amino acid sequence with tyrosine (Y), lysine (K), and/or valine residues. The complex of the peptide with a major histocompatibility complex (WHC) class II HLA-DE protein is involved in modulating an immune response. (I) has antiinflammatory and neuroprotective activities, and can be used as a MHC class II protein inhibitor. The compositions comprising the peptides are useful for treating demyelinating diseases such as multiple sclerosis, post-viral encephalomyelitis, a post-vaccine demyelinating condition, and a side effect of administering an anti-tumour necrosis factor agents. The peptide further inhibits proliferation of autoantigen-specific HLA-DEZ-restricted T cell clones. ABB52207 to
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                                                                                                                                                                                                                                                                                                                                                                                     Human leukocyte antigen; HLA; major histocompatibility complex; MHC; HLA-DR2; MHC class II DR-2 molecule; demyelinating; multiple sclerosis; immune response; antiinflammatory; neuroprotective; proliferation; MHC class II protein inhibitor; demyelinating disease; inhibition; post-viral encephalomyelitis; post-vaccine demyelinating condition; anti-tumour necrosis factor agent.
                                                                                                                                                                                                                                                                                                            HLA-DR2 molecule binding peptide SEQ ID NO:90.
                                                                             ABPS2296 standard; peptide; 17 AA.
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RESULT 15
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Gaps ; 75.0%; Score 57; DB 5; Length 17; 80.0%; Pred. No. 0.021; Live 1; Mismatches 2; Indels Best Local Similarity 80.0 Matches 12; Conservative Query Match

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Search completed: March 31, 2005, 02:35:28 Job time: 89.7903 secs

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                  March 31, 2005, 02:26:53 ; Search time 22.9839 Seconds (without alignments) 48.718 Million cell updates/sec
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| /cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
| /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
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GenCore version 5.1.6
(c) 1993 - 2005 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                                                                         513545 segs, 74649064 residues
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Listing first 45 summaries
                                                                                      - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Match
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Perfect score:
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Maximum DB
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Score Match Length DB ID

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52.6 2471 4 US-09-101-597-1
52.7 3 US-09-101-597-1
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1 EKPKFEAYKAAAAP 14

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Sequence Sequence Sequence Sequence

3-09-949-016-7245 3-10-029-180-76 3-09-902-540-15480 3-09-543-681A-7747

US-07-977-434-6 US-08-458-819-6

Sequence

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		on NUCLEIC ACIDS, ELATED METHODS	Length ; 6; Inde
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US91-0703 88-073-384 88-484-355 88-481-056 88-481-056 88-481-056 88-757-653 88-759-489 88-823-516 88-759-038 89-759-038	ALIGNMENTS	ve as 'R	re 40; DB d. No. 3.6 Mismatches
DCT-US91-070 US-08-073-38 US-08-254-35 US-08-481-04 US-08-471-06 US-08-471-06 US-08-757-65 US-08-757-65 US-08-823-51 US-08-823-51 US-08-823-31 US-08-823-31 US-08-682-93 US-08-756-38 US-08-682-95 US-08-682-95 US-08-756-31 US-08-682-95 US-08-756-31 US-08-756-31 US-08-756-31 US-08-756-31 US-08-756-31 US-08-756-31 US-08-756-31 US-08-756-31 US-08-756-31 US-08-756-31 US-08-756-31 US-08-756-31 US-08-756-31 US-08-756-31 US-08-756-31	ALIC	185432 188, Spyr 198, La J. 198, AND 19	Score Pred.
		pplication US/08185432 MATLOWS: Artavania-Tsakonas, Sp Busseau, Isabelle Busseau, Isabelle Busseau, Isabelle Busseau, Isabelle Busseau, Isabelle Busseau, Isabelle Matsuno, Kenji Matsuno, Kenji Matsuno, Renji Matsuno, Renji Matsuno, Renji Matsuno, Berrinx PROTEI ENTION: DELIEX PROTEI PENTION: DELIEX PROTEI PENTION: A'YOK U.S.A. 15.Avenue of the Amer VYORK U.S.A. 16-2711 BERIOPO disk U.S.A. 16-2711 BERIOPO disk U.S.A. 16-2711 BERIOPO disk U.S.A. 17-2710 DARA: 18-21-34N-1994 TION: S.30 TIONERER: US/08/185,44 TION INFORMATION: 10-0CKT NUMBER: 7326-0 ATION INFORMATION: 10-0C	
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a a a a a a a a a a a a a a a a a a a		ULT 1 08-185-432-16 equence 16, Application US/08185 atent No. 575652 APPLICANT: Artavania-Tsakonas APPLICANT: Buseau, Isabelle APPLICANT: Buseau, Isabelle APPLICANT: Matsuno, Kenji TITLE OF INVENTION: DELTEX PR TITLE OF INVENTION: DELTEX PR TITLE OF INVENTION: DELTEX PR TITLE OF INVENTION: ANTIBODIS NUMBER OF SEQUENCES: 23 CORRESPONDENCE ADDRESS: EDMONDS STREET: 1155 Avenue of the CITY: New York CUNTRY: U.S.A. ZIP: 10036-2711 COMPUTER: IBM PC compatible COMPUTER: IBM PC compatible COMPUTER: TEMPON US/08/1 FILING DATE: 21-JAN-1994 CLASSIFICATION NUMBER: 18/09/1 FILING DATE: 21-JAN-1994 CLASSIFICATION NUMBER: 18/09/1 FILING DATE: 21-JAN-1994 CLASSIFICATION NUMBER: 18/09/1 TELEFROME CHARACTERISTICS: LENGTH: 2471 amino acids TYPE: TYPE: TYPE: DYPE: DYPOLEIN	ch 1 Sir 7;
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                                                                                    US-08-083-590A-19

Sequence 19, Application US/08083590A

Sequence 19, Application US/08083590A

GENERAL INFORMATION:

APPLICANT: Artevanis-Tsakonas, S. et al.

TITLE OF INVENTION: Therapeutic And Diagnostic Methods

TITLE OF INVENTION: And Compositions Based On No. 5786158ch Proteins And

TITLE OF INVENTION: Nucleic Acids

NUMBER OF SEQUENCES: 21

CORRESPONDENCE ADDRESS:

ADDRESSER: Pennie & Edmonds

STREET: 115 Avenue of the Americas
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Sequence 19, Application US/08532384
Patent No. 6083904
GENERAL INFORMATION:
APPLICANT: Artavania-Tsakonas, S. et al.
TITLE OF INVENTION: Therapeutic And Diagnostic Methods
TITLE OF INVENTION: And Compositions Based On No. 6083904ch Proteins And
TITLE OF INVENTION: Nucleic Acids
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
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Pred. No. 3.6e+02;
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/083,590A
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JUNE 435
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STREET: 1155 Avenue of the Americas
CITY: New York
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FRP: 7326-015
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NAME: Misrock, S. Leslie
REGISTRATION NUMBER: 18,872
REFRENCE/DOCKET NUMBER: 7326
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212 790-9090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEFAX: 212 8698864/9741
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
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50.0%;
                  850 ESPNFESYTCLCAP 863
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Best Local Similarity 50.04
Ti Conservative
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STRANDEDNESS: si
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: U.S.A.
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CITY: New York
STATE: New York
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CLASSIFICATION:
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ZIP: 10036
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Sequence 1, Application US/08899232
| Patent No. 645650
| GENERAL INFORMATION:
| APPLICANT: Artavanis-Teakonas, Spyridon
| APPLICANT: Attavanis-Teakonas, Spyridon
| TITLE OF INVENTION: ACTIVATED FORMS OF NOTCH AND METHODS BASED THEREON
| TITLE OF INVENTION: ACTIVATED FORMS OF NOTCH AND METHODS BASED THEREON
| TITLE OF INVENTION: NUMBER: US/08/899,232
| CURRENT FILING DATE: 1997-07-23
| NUMBER OF SEQ ID NOS: 4
| SOFTWARE: PatentIn Ver. 2.0
| SEQ ID NO 1
| LENGTH: 2471
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/532,384
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1; Mismatches
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                                                                                                                                                                                                                                                                            NAME: Misrock, S. Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 7326-015
TELEPHONE: 212 790-9090
TELEPAX: 212 8698864/9741
TELEPAX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
                                                                                                                                      FILING DATE:
CLASSIFICATION: 424
RIOR APPLICATION DATA:
APPLICATION NUMBER: 08/083,590
FILING DATE: 25-JUN-1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 1, Application US/09121457; Patent No. 6692019; GENERAL INFORMATION: APPLICANT: Arevanis-Tsakonas, S. APPLICANT: Qi, H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 2471 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 850 ESPNFESYTCLCAP 863
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Best Local Similarity 50.0°
Matches 7; Conservative
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Best Local Similarity 50.0°
Matches 7; Conservative
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MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        single
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ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: amino acid
STRANDEDNESS: si
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-08-532-384-19
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US-08-899-232-1
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US-09-121-457-1
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1 EKPKFEAYKAAAPA 15
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Best Local Similarity
7; Conserv?
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                                                                                   ; TYPE: PRT
; ORGANISM: Human
US-09-949-016-9547
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APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF FILE REPERENCE: CL001307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT PILING DATE: 2000-10-20
PRIOR PILING DATE: 2000-10-20
PRIOR PILING DATE: 2000-10-3
PRIOR FILING DATE: 2000-10-3
PRIOR FILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-0-09-08
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US-09-513-999C-5101
; Sequence 5101, Application US/09513999C
; Patent No. 6783961
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
; Patent No. 6783961
; FILE REFERENCE: 59.US2.REG
; CURRENT FILING DATE: 2000-02-24
; FRIOR APPLICATION NUMBER: US 60/122,487
; PRIOR PILING DATE: 1999-02-8
; NUMBER OF SEQ ID NOS: 36681
; SOFTWARE: Patent.pm
; SEQ ID NO 5101
; LENGTH: 75
APPLICANT: Rand, M.
TITLE OF INVENTION: ACTIVATED FORMS OF NOTCH AND METHODS BASED THEREON
TITLE REFERENCE: 7326-073
CURRENT APPLICATION NUMBER: US/09/121,457
CURRENT FILING DATE: 1998-07-23
EARLIER APPLICATION NUMBER: 08/899,232
BARLIER PILING DATE: 1997-07-23
NUMBER OF SEQ ID NOS: 4
SOFTWARE: PATENTIN Ver. 2.0
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Pred. No. 3.6e+02;
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; Patent No. 6812339
                                                                                                                                                                                                                                                                                                    52.6%;
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64.3%;
                                                                                                                                                                                                                                                                                                                                                                                                         850 ESPNFESYTCLCAP 863
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Best Local Similarity 64.5.
                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 50.0
Matches 7; Conservative
                                                                                                                                                                                                                    TYPE: PRT
ORGANISM: Homo sapiens
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ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-09-513-999C-5101
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US-09-949-016-9547
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Second 1832, Application US/09252991A
Facent No. 6551795
GENERAL INFORMATION:
TITLE OF INVENTION: WUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: WUCLEIC ACID AND THERAPEUTICS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: MUMBER: US/09/252,991A
CURRENT APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1999-02-18
PRIOR FILING DATE: 1998-02-18
PRIOR FILING DATE: 1998-02-18
PRIOR FILING DATE: 1998-02-18
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 18932
LENGTH: 297
                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
APPLICANT: Gary Breton et. al
APPLICANT: Gary Breton et. al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
TITLE OF INVENTION: NUCLEUR FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 2709.2004001
CURRENT PERLICATION NUMBER: US/09/489,039A
CURRENT FILING DATE: 2000-01-27
PRIOR PELICATION NUMBER: US 60/117,747
PRIOR FILING DATE: 1999-01-29
NUMBER OF SEQ ID NOS: 14342
SEQ ID NO 7214
LENGTH: 243
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                                                                                                                                                                   Length 222;
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                                                                                                                                                                   DB 4;
38;
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42;
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NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 9547
LENGTH: 222
                                                                                                                                                                   Score 39;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                               ; Sequence 7214, Application US/09489039A; Patent No. 6610836
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-18932
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORGANISM: Klebsiella pneumoniae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 51.3%;
58.3%;
                                                                                                                                                                   51.3%;
64.3%;
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Best Local Similarity 46.77
Matches 7; Conservative
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Best Local Similarity 64.3
Matches 9; Conservative
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Gaps

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Length 1402;
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APPLICANT: Michelmore, Richard W.
APPLICANT: Shen, Kathy
APPLICANT: Shen, Kathy
APPLICANT: Mayers, Blake
TITLE OF INVENTION: Procedures and Materials for
TITLE OF INVENTION: Conferring Pest Resistance in Plants
NUMBER OF SEQUENCES: 140
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                   2; Indels
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SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/004,838
FILING DATE: 09-JAN-1998
CLASSIFICATION: 800
PRIOR APPLICATION: 800
PRIOR APPLICATION NUMBER: US 08/781,734
FILING DATE: 10-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Einhorn, Gregory P.
REGISTRATION NUMBER: 38,440
REFERENCE/DOCKET NUMBER: 023070-078810US
TELEPHONE: (415) 576-0300
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTER(STICS:
SEQUENCE CHARACTER(STICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE: Townsend and Townsend and Crew LLP STREET: Two Embarcadero Center, Bighth Floor CITY: San Francisco STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; NAME/KEY: -
; LOCATION: 1..1402
; CTRER INFORMATION: /note= "RLG1A amino acids"
US-09-004-838-11
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Pred. No. 2.9e+02;
                                                                                                                                                                                                                                                                                                                                                1; Mismatches
  CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
SEQ ID NO 27869
LENGTH: 469
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 11, Application US/09004838 Patent No. 6350933
                                                                                                                                                                                                                         ) ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-27869
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Best Local Similarity 72./-
8; Conservative
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181 FERFKAAAYPA 191
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 USA
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US-09-004-838-11
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Patent No. 6551795
GENERAL No. 6551795
GENERAL MARC J. Rubenfield et al.
TITLE OF INVENTION: ARRUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
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                                                                                                       JUNE - 09-004-838-14

Sequence 14, Application US/09004838

Sequence 14, Application US/09004838

GENERAL INFORMATION:
APPLICANT: Michelmore, Richard W.
APPLICANT: Shen, Kathy
APPLICANT: Shen, Kathy
APPLICANT: Shen, Kathy
TITLE OF INVENTION: Procedures and Materials for
TITLE OF INVENTION: Conferring Pest Resistance in Plants
NUMBER OF SEQUENCES: 140

CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 39; DB 3; Length 314;
Pred. No. 55;
2; Mismatches 2; Indels
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MEDIUM TYPE: Floppy disk
COMPUTER: The PC compartible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/004,838
FILING DATE: 09-JAN-1998
CLLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/781,734
FILING DATE: 10-JAN-1997
ATTORNEY/AGENT INPORMATION:
NAME: Einhorn, Gregory P.
REGISTRATION NUMBER: 38,440
REFERENCE/DOCKET NUMBER: 38,440
REFERENCE/DOCKET NUMBER: 38,440
REFERENCE/DOCKET NUMBER: 38,440
REFERENCE/DOCKET NUMBER: 356-0200
TELECHOMMUNICATION INPORMATION:
TELECOMMUNICATION INPORMATION:
TELECOMMUNICATION INPORMATION:
TELECOMMUNICATION INPORMATION:
TELECOMMUNICATION INPORMATION:
TELECOMMUNICATION INPORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
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STREET: Two Embarcadero Center, Bighth Floor
CITY: San Francisco
STATE: California
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; OTHER INFORMATION: /note= "RLG1D amino acids"
US-09-004-838-14
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INFORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 314 amino acids
TYPE: amino acid
STRANDEDNESS:
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Best Local Similarity 63.0
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114 EKPKIERYEAS 124
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY: USA
ZIP: 94111-3834
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Sequence 1752, Application US/09248796A

Sequence 1752, Application US/09248796A

Patent No. 6747137

GENERAL INFORMATION:
TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
CURRENT APPLICATION NUMBER: US/09/248,796A

CURRENT FILING DATE: 1999-02-13
PRIOR FILING DATE: 1998-02-13
PRIOR FILING DATE: 1998-02-13
NUMBER OF SEQ ID NOS: 28208

SEQ ID NO 17592
LENGTH: 260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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Pred. No. 67;
0; Mismatches 1; Indels
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Job time : 23.9839 secs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 87.5%;
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                        ; TYPE: PRT
; ORGANISM: Candida albicans
US-09-248-796A-17592
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US-09-248-796A-20648

US-09-248-796A-20648

Sequence 20648, Application US/09248796A

Factor No. 6747137

GENERAL INFORMATION:
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN
TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196-132

CURRENT APPLICATION NUMBER: US 60/074,725

FRIOR APPLICATION NUMBER: US 60/074,725

FRIOR APPLICATION NUMBER: US 60/074,725

FRIOR PLING DATE: 1998-02-13

FRIOR FILING DATE: 1998-02-13

FRIOR FILING DATE: 1998-08-13

NUMBER OF SEQ ID NOS: 28208

SEQ ID NO 20648
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APPLICANT: Goldman, Barry S.
APPLICANT: Hinkle, Gregory J.
APPLICANT: Hinkle, Gregory J.
APPLICANT: Hinkle, Gregory J.
APPLICANT: Miegand, Roger C.
TITLE OF INVENTION: Myxcoccus xanthus Genome Sequences and Uses Thereof
FILE REFERENCE: 38-10 (15649) B
CURRENT APPLICATION NUMBER: US/09/902,540
CURRENT APLICATION NUMBER: 60/217,883
PRIOR PILING DATE: 2000-07-10
NUMBER OF SEQ ID NOS: 16825
SEQ ID NO 16512.
    Gaps
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Pred. No. 15;
    2; Indels
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  2; Mismatches
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US-09-902-540-16512
; Sequence 16512, Application US/09902540
; Patent No. 6833447
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; ORGANISM: Myxococcus xanthus
US-09-902-540-16512
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ORGANISM: Candida albicans
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Best Local Similarity 72.7
Matches 8; Conservative
7; Conservative
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515 EKPKIERYEAS 525
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US-10-056-583-85
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                                                                                                                                                                            March 31, 2005, 02:29:23 ; Search time 66.5323 Seconds (without alignments) 74.648 Million cell updates/sec
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Sequence 85,
Sequence 98,
Sequence 93,
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1: /cgn2_6/ptodata/2/pubpaa/USO7_PUBCOMB.pep:*

2: /cgn2_6/ptodata/2/pubpaa/PCT NEW PUB.pep:*

3: /cgn2_6/ptodata/2/pubpaa/USO6_NEW PUB.pep:*

4: /cgn2_6/ptodata/2/pubpaa/USO6_PUBCOMB.pep:*

5: /cgn2_6/ptodata/2/pubpaa/USO6_PUBCOMB.pep:*

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8: /cgn2_6/ptodata/2/pubpaa/USO8_PUBCOMB.pep:*

9: /cgn2_6/ptodata/2/pubpaa/USO8_PUBCOMB.pep:*

10: /cgn2_6/ptodata/2/pubpaa/USO8_PUBCOMB.pep:*

11: /cgn2_6/ptodata/2/pubpaa/USO9_PUBCOMB.pep:*

11: /cgn2_6/ptodata/2/pubpaa/USO9_PUBCOMB.pep:*

11: /cgn2_6/ptodata/2/pubpaa/USO9_NEW PUB.pep:*

12: /cgn2_6/ptodata/2/pubpaa/USO0_PUBCOMB.pep:*

13: /cgn2_6/ptodata/2/pubpaa/USO0_PUBCOMB.pep:*

14: /cgn2_6/ptodata/2/pubpaa/USO0_PUBCOMB.pep:*

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19: /cgn2_6/ptodata/2/pubpaa/USO0_PUBCOMB.pep:*

10: /cgn2_6/ptodata/2/pubpaa/USO0_PUBCOMB.pep:*

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10: /cgn2_6/ptodata/2/pubpaa/USO0_NEW_PUB.pep:*
GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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US-10-056-583-95
US-10-056-583-93
US-10-056-583-97
US-10-056-583-84
US-10-056-583-86
US-10-056-583-96
US-10-056-583-96
US-10-056-583-96
US-10-056-583-99
US-10-056-583-99
US-10-056-583-99
US-10-056-583-93
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                               - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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seq length: 200000000
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84.2
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Maximum DB
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US-10-056-583-90
US-10-056-583-89
US-10-056-583-87
US-10-056-583-87
US-10-056-583-67
US-10-056-583-66
US-10-056-583-57
US-10-056-583-51
US-10-056-583-43
US-10-056-583-43
US-10-056-583-43
US-10-056-583-45
US-10-056-583-45
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US-10-056-583-63
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ALIGNMENTS

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Gaps
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Sequence 91. Application US/10056583
Sequence 91. Application US/10056583
GENERAL INFORMATION:
APPLICANT: Presidents and Fellows of Harvard College
APPLICANT: Pridkis-Harreli, Masha
TITLE OF INVENTION: THERAPEUTIC PEPTIDES FOR DEMYELINATING
TITLE OF INVENTION: CONDITIONS
TITLE OF INVENTION: 20659-01-24
FOURENT APPLICATION NUMBER: 60,263,569
PRIOR FILING DATE: 2001-01-24
NUMBER OF SEQ ID NOS: 99
SEQ ID NO 91
LENGTH: 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                100.0%; Score 76; DB 14; Length 15; 100.0%; Pred. No. 2.5e-06;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; OTHER INFORMATION: The peptide was designed and synthesized US-10-056-583-91
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                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: PRT
ORGANISM: Artificial Sequence
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Best Local Similarity 100.0
Matches 15; Conservative
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Sequence 97, Application US/10056583

Sequence 97, Application US/10056583

Publication No. US20030064915A1

GENERAL INFORMATION:

APPLICANT: Presidents and Fellows of Harvard College

APPLICANT: Pridkis Harreli, Masha

TITLE OF INVENTION: THERAPEUTIC PEPTIDES FOR DEMYELINATING

TITLE OF INVENTION: THERAPEUTIC PEPTIDES FOR DEMYELINATING

TITLE OF INVENTION: THERAPEUTIC PEPTIDES FOR DEMYELINATING

TITLE OF INVENTION: THERAPEUTIC PEPTIDES

CURRENT APPLICATION NUMBER: US/10/056,583

CURRENT PILING DATE: 2002-01-24

PRIOR PILING DATE: 2001-01-24

NUMBER OF SEQ ID NOS: 99

SOFTWARE: PSECSEQ for Windows Version 4.0

SEQ ID NO 97

LENGTH: 17
     APPLICANT: Fridkis-Hareli, Masha
TITLE OF INVENTION: THERAPEUTIC PEPTIDES FOR DEMYELINATING
TITLE OF INVENTION: CONDITIONS
FILE REPERBACE: 2655-017
CURRENT FILING DATE: 2002-01-24
PRIOR APPLICATION NUMBER: 60/263,569
PRIOR PELICHG DATE: 2001-01-24
NUMBER OF SEQ ID NOS: 99
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 93
LENGTH: 15
                                                                                                                                                                                                                                                                                                                                                ORGANISM: Artificial Sequence Franciscopersons of Paralysms OTHER INFORMATION: The peptide was designed and synthesized. US-10-056-583-93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; OTHER INFORMATION: The peptide was designed and synthesized.
US-10-056-583-97
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Best Local Similarity 93.3%; Pred. No. 6.9e-05;
Matches 14; Conservative 0; Mismatches 1; Indels
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Publication No. US20030064915A1
GENERAL INFORMATION:
APPLICANT: Presidents and Fellows of Harvard College
APPLICANT: Fridxia-Hareli, Masha
TITLE OF INVENTION: THERAPEUTIC PEPTIDES FOR DEMYELINATING
TITLE OF INVENTION: CONDITIONS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
90.8%; Score 69; DB 14;
Best Local Similarity 93.3%; Pred. No. 4.1e-05;
Matches 14; Conservative 0; Mismatches 1.
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                                                                                                APPLICANT: Stroninger, Jack L.
APPLICANT: Fridkis-Hareli, Masha,
TITLE OF INVENTION: THERAPEUTC PEPTIDES FOR DEMYELINATING
TITLE OF INVENTION: CONDITIONS
FILE REFERENCE: 24655-017
CURRENT APPLICATION NUMBER: US/10/056,583
CURRENT FILING DATE: 2002-01-24
PRIOR APPLICATION NUMBER: 60/263,569
PRIOR APPLICATION NUMBER: 60/263,569
NUMBER OF SEQ ID NOS: 99
SOFTWARE: FastSEQ for Mindows Version 4.0
SEQ ID NO 85
LENGTH: 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-10-056-583-98

Sequence 98, Application US/10056583

Publication No. US20030064915A1

GENERAL INFORMATION:
APPLICANT: Presidents and Fellows of Harvard College
APPLICANT: Strominger, Jack L.
TITLE OF INVENTION: THERAPEUTIC PEPTIDES FOR DEMYELINATING
TITLE OF INVENTION: CONDITIONS
FILE REFERENCE: 24655-017

CURRENT APPLICATION NUMBER: 60/263,569

PRIOR PELLING DATE: 2001-01-24

NUMBER OF SEQ ID NOS: 99

SOFTWARE: FRASESEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; OTHER INFORMATION: The peptide was designed and synthesized. US-10-056-583-85
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     96.1%; Score 73; DB 14; Length 15; 93.3%; Pred. No. 8.2e-06; tive 1; Mismatches 0; Indels
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Sequence 85, Application US/10056583
Publication No. US20030064915A1
GENERAL INFORMATION:
APPLICANT: Presidents and Fellows of Harvard College
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Publication No. US20030064915A1
GENERAL INFORMATION:
APPLICANT: Presidents and Fellows of Harvard College
APPLICANT: Strominger, Jack L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Mismatches
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ORGANISM: Artificial Sequence
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nes 14; Conserv
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US-10-056-583-93
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LENGTH: 15
TYPE: PRT
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FILE REFERENCE: 24655-017 CURRENT APPLICATION NUMBER: US/10/056,583

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US-10-056-583-99
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Sequence 86, Application US/10056583;
Publication No. US20030064915A1;
GENERAL INFORMATION:
APPLICANT: Presidents and Fellows of Harvard College
APPLICANT: Strominger, Jack L.
TITLE OF INVENTION: THERAPEUTIC PEPTIDES FOR DEMYELINATING
TITLE OF INVENTION: CONDITIONS
FILE REFERENCE: 24655-017;
CURRENT APPLICATION NUMBER: US/10/056,583;
CURRENT FILING DATE: 2002-01-24;
PRIOR PLLICATION NUMBER: 60/263,569;
PRIOR PLLING DATE: 2001-01-24;
NUMBER OF SEQ ID NOS: 99;
SOFTWARE: PESCEEQ for Windows Version 4.0
                                                                                                                                                                                                                   ; OTHER INFORMATION: The peptide was designed and synthesized.
US-10-056-583-84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; OTHER INFORMATION: The peptide was designed and synthesized US-10-056-583-86
                                                                                                                                                                                                                                                                                    88.2%; Score 67; DB 14; Length 15; 86.7%; Pred. No. 9e-05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 67; DB 14; Length 15;
Pred. No. 9e-05;
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APPLICANT: Strominger, Jack L.
APPLICANT: Pridtis-Hazeli, Masha
TITLE OF INVENTION: THERAPEUTIC PEPTIDES FOR DEMYELINATING
TITLE OF INVENTION: CONDITIONS
FILE REFERENCE: 24655-017
CURRENT APPLICATION NUMBER: US/10/056,583
CURRENT APPLICATION NUMBER: 60/263,569
PRIOR PILING DATE: 2001-01-24
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CURRENT FILING DATE: 2002-01-24
PRIOR APPLICATION NUMBER: 60/263,569
PRIOR FILING DATE: 2001-01-24
NUMBER OF SEQ ID NOS: 99
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 84
LENGTH: 15
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SOFTWARE: FastSEQ for Windows Version 4.0
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ORGANISM: Artificial Sequence
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ORGANISM: Artificial Sequence
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Best Local Similarity 86.7
Matches 13; Conservative
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Matches 13; Conservative
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US-10-056-583-86
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APPLICANT: Strominger, Jack L.
APPLICANT: Strominger, Jack L.
APPLICANT: Fridkis-Hareli, Masha
TITLE OF INVENTION: THERAPEUTIC PEPTIDES FOR DEMYELINATING
TITLE OF INVENTION: CONDITIONS
FILE REPERENCE: 24655-017
CURRENT APPLICATION NUMBER: US/10/056,583
CURRENT FILING DATE: 2002-01-24
PRIOR APPLICATION NUMBER: 60/263,569
PRIOR PILING DATE: 2001-01-24
NUMBER OF SEQ ID NOS: 99
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 94
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APPLICANT: Strominger, Jack L.
APPLICANT: Fridkis-Hareli, Masha
TITLE OF INVENTION: THERAPEUTIC PEPTIDES FOR DEMYELINATING
TITLE OF INVENTION: THERAPEUTIC PEPTIDES FOR DEMYELINATING
TITLE OF INVENTION: THERAPEUTIC CONDITIONS
FILE REPERENCE: 24655-017
CURRENT APPLICATION NUMBER: US/10/056,583
CURRENT FILING DATE: 2002-01-24
PRIOR FILING DATE: 2001-01-24
NUMBER OF SEQ ID NOS: 99
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 99
LENGTH: 15
                                                                                                                       ; OTHER INFORMATION: The peptide was designed and synthesized.
US-10-056-583-96
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86.7%; Pred. No. 0.00044;
iive 1; Mismatches 1; Indels
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Publication No. US20030064915A1
GENERAL INFORMATION:
APPLICANT: Presidents and Fellows of Harvard College
                                                                                                                                                                                                                   Score 64; DB 14;
Pred. No. 0.00034;
                                                                                                                                                                                                                                                                           Mismatches
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SEQ ID NO 96
LENGTH: 17
TYPE: PRT
ORGANISM: Artificial Sequence
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Best Local Similarity 86.7%;
Matches 13; Conservative
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1 EKPKEEAFKAAAPA 15
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Matches 13; Conservative
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APPLICANT: Strominger, Jack L.
APPLICANT: Fridkis-Hareli, Masha
TITLE OF INVENTION: THERAPEUTIC PEPTIDES FOR DEMYELINATING
TITLE OF INVENTION: CONDITIONS
FILE REPREMENT
CURRENT APPLICATION NUMBER: US/10/056,583
CURRENT PILING DATE: 2002-01-24
PRIOR APPLICATION NUMBER: 60/263,569
PRIOR FILING DATE: 2001-01-4
NUMBER OF SEQ ID NOS: 99
SOOTWARR: FastSEQ for Windows Version 4.0
SEQ ID NO 88
LENGTH: 17
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APPLICANT: Strominger, Jack L.
APPLICANT: Strominger, Jack L.
APPLICANT: Strominger, Jack L.
APPLICANT: Strominger, Jack L.
APPLICANT: Strikis-Harell, Masha
TITLE OF INVENTION: THERAPEUTIC PEPTIDES FOR DEMYELINATING
TITLE OF INVENTION: CONDITIONS
FILE REFERENCE: 24655-017
CURRENT APPLICATION NUMBER: 18/10/056,583
FURNENT FILING DATE: 2002-01-24
PRIOR FILING DATE: 2001-01-24
       Indels
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Pred. No. 0.0056;
    Mismatches
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 90
LENGTH: 17
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US-10-056-583-90
; Sequence 90, Application US/10056583
; Publication No. US20030064915A1
; GENERAL INFORMATION:
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1 EAPAYKAYKAAAAPA 15
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Best Local Similarity 80.04
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Best Local Similarity 80.0
Matches 12; Conservative
    11; Conservative
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                                                                                                                       Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 12
US-10-056-583-83
Sequence 83, Application US/10056583
Sequence 83, Application US/10056583
Publication No. US20030064915A1
GENERAL INFORMATION:
APPLICANT: Presidents and Fellows of Harvard College
TYPE OF INVENTION: THERAPEUTIC PEPTIDES FOR DEMYELINATING
TITLE OF INVENTION: CONDITIONS
FILE REFERENCE: ZGOTOTIONS
TITLE OF INVENTION: CONDITIONS
CURRENT APPLICATION NUMBER: US/10/056,583
CURRENT FILING DATE: 2002-01-24
PRIOR FILING DATE: 2001-01-24
                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Presidents and Fellows of Harvard College
APPLICANT: Strominger, Jack L.
APPLICANT: Strominger, Jack L.
APPLICANT: Strickis-Harsli, Masha
TITLE OF INVENTION: THERABEUTIC PEPTIDES FOR DEMYELINATING
TITLE OF INVENTION: CONDITIONS
FILE REFERENCE: 24655-017
CURRENT PELING DATE: 2002-01-24
PRIOR PILING DATE: 2001-01-24
PRIOR APPLICATION NUMBER: 60/263,569
PRIOR APPLICATION NUMBER: 60/263,569
PRIOR PILING DATE: 2001-01-24
NUMBER OF SEQ ID NOS: 99
SOFTWARE: FRSESEQ for Windows Version 4.0
; OTHER INFORMATION: The peptide was designed and synthesized.
US-10-056-583-99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; OTHER INFORMATION: The peptide was designed and synthesized US-10-056-583-83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; OTHER INFORMATION: The peptide was designed and synthesized US-10-056-583-65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 75.0%; Score 57; DB 14; Length 15; Best Local Similarity 80.0%; Pred. No. 0.0048; Matches 12; Conservative 1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 57; DB 14; Length 15;
Pred. No. 0.0048;
                                                                         Length 15
                                                                      Score 63; DB 14;
Pred. No. 0.00044;
                                                                                                                    Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQ ID NOS: 99
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 83
LENGTH: 15
TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                      US-10-056-583-65; Sequence 65, Application US/10056583; Publication No. US20030064915A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        75.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQ ID NO 65
LENGTH: 15
TYBE: PRT
ORGANISM: Artificial Sequence
                                                                    Query Match 82.9%;
Best Local Similarity 86.7%;
Matches 13; Conservative
                                                                                                                                                                                                            1 EAPKVEAYKAAAPA 15
                                                                                                                                                                   1 EKPKFEAYKAAAPA 15
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Best Local Similarity
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Gaps

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US-10-056-583-89

Sequence 89, Application US/10056583

Sequence 89, Application WS/10056583

Sequence 89, Application No. US20030064915A1

GENERAL INFORMATION:
APPLICANT: Stronminger, Jack L.
APPLICANT: Stronminger, Jack L.
APPLICANT: Fridkis-Hareli, Masha
TITLE OF INVENTION: THERAPEUTIC PEPTIDES FOR DEMYELINATING
TITLE OF INVENTION: THERAPEUTIC PEPTIDES FOR DEMYELINATING
FILE REFERENCE: 24655-017
CURRENT ILLING DATE: 2002-01-24
CURRENT FILING DATE: 2001-01-24
NUMBER OF SEQ ID NOS: 99
SEQ ID NO 89
IEMOTH: 19
IE
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Search completed: March 31, 2005, 02:48:48 Job time : 66.5323 secs

1 EKPKFEAYKAAAAPA 15 || |- || || || || || || 3 3 EKAKYEAYKAAAAAA 17

8 8

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GenCore version 5.1.6 Copyright (c) 1993 - 2005 Compugen Ltd.

- protein search, using sw model OM protein March 31, 2005, 02:26:17; Search time 17.9032 Seconds (without alignments) 80.614 Million cell updates/sec Run on:

1 EKPKFEAYKAAAAPA 15 US-10-056-583A-91 76 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283416 seqs, 96216763 residues Searched:

283416 Total number of hits satisfying chosen parameters:

seq length: 0 seq length: 200000000 Minimum DB Maximum DB

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 su

PIR 79:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:* Database

summaries

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

		de			SUMMARIES	
Result No.	Score	Query Match	Length	DB	ID	Description
	44	57.9	193	į a	MOMS4E	myosin alkali ligh
7	43	26.6	306	~	G96014	hypothetical profe
m	43	56.6	336	7	B81081	tryptophanyl-tRNA
4	43	9.95	336	•	E81863	tryptophan-tRNA li
Ŋ	43	56.6	389	~	G87332	hypothetical prote
9	42.5	55.9	316	7	T14643	1-aminocyclopropan
7	42	55.3	270	N	T31225	traf protein homol
œ	42	55.3	554	~	868365	(+)-delta-cadinene
σ	42	55.3	554	~	S68366	(+)-delta-cadinene
10	41	53.9	185	٦	MOCH4E	alkali
11	41	53.9	193	٦	MORT4E	myosin alkali ligh
12	41	53.9	194	7	T14644	1-aminocyclopropan
13	41	53.9	200	7	T48130	hypothetical prote
14	41	53.9	216	•	AG3508	transporter BMEI20
15	41	53.9	398	7	T21061	
16	40	52.6	321	~	T07922	probable 1-aminocy
17	40	52.6	461	7	AI3358	pyruvate dehydroge
18	40	52.6	765	~	T15447	hypothetical prote
19	40	52.6	891	~	AC3384	ø
20	39	51.3	73	7	S40015	phd protein - phag
21	39	51.3	114	7	G81353	hypothetical prote
22	39	51.3	168	~	A45943	vitelline membrane
23	39	51.3	197	-	MOHU4E	myosin alkali ligh
24	39	51.3	215	~	AG3392	maleylpyruvate iso
25	39	51.3	239	-	C44954	fumarate reductase
26	39	51.3	310	7	T09733	1-aminocyclopropan
27	39		321	7	T02754	probable 1-aminocy
28	39	51.3	334	Н	DEQYG	glyceraldehyde-3-p
53	39	51.3	334	~	E75153	glyceraldehyde 3-p

probable glycerald phosphate-binding probable zinc prot	C-22 sterol desatu hypothetical prote probable cell surf probable oxidoredu	hypothetical prote hypothetical prote 50s ribosomal prot 50s ribosomal prot	homeotic protein H ABC transporter AT homeotic protein H	1-aminocyclopropan hypothetical prote
G71194 C70473 D83598	S54015 T29657 AE1479 C95401	T00039 G97151 F97683 AF2908	IS0145 E86691 A43562	T10817 B86255
0 H 0	0000	0000	000	0 0
334 337 465	538 586 656 810	906 50 179	188 269 289	308 320
51.3 51.3 51.3	51.3 51.3 51.3	50.07	20.00	50.0
6 6 6 6 7 7 7	5 5 5 5 5 6 6 6 6 6	38 38 38 38	8888	38
30 32	2 2 2 2 3 3 4 3 4 3 4 4 4 4 4 4 4 4 4 4	3 3 3 4 4 5 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6	4 4 4 1 2 6	4 4 5

ALIGNMENTS

myosin alkali light chain 4, embryonic and atrial - mouse N;Alternate names: MLCIA; MLCIemb; myosin L1 catalytic light chain, atrial MOMS4E

C;Species: Mus musculus (house mouse)
C;Date: 31-Mar-1990 #sequence_revision 03-Oct-1995 #text_change 09-Jul-2004
C;Accession: A31114; S01944
R;Barton, P.J.R.; Robert, B.; Cohen, A.; Garner, I.; Sassoon, D.; Weydert, A.; Buckingha J. Biol. Chem. 263, 12669-12676, 1988
A;Title: Structure and sequence of the myosin alkali light chain gene expressed in adult A;Reference number: A31114; MUID:88315068; PMID:2842339

A;Accession: A31114
A;Molecule type: DNA
A;Molecule type: DNA
A;Molecule type: DNA
A;Rosidues: 1-193 < dAR>
A;Cross-references: UNIPROT:P09541; GB:M20772; GB:J03932; GB:M19435; NID:g199731; PIDN:A
A;Cross-references: UNIPROT:P09541; GB:M20772; GB:J03932; GB:M19435; NID:g199731; PIDN:A
R;Cohen, A:; Barton, P.J.R.; Robert, B.; Garner, I.; Alonso, S.; Buckingham, M.E.
R;Cohen, A:; Barton, P.J.R.; Robert, B.; Garner, I.; Alonso, S.; Buckingham, M.E.
A;Title: Promoter analysis of myosin alkali light chain genes expressed in mouse striate
A;Reference number: S01944; MUID:89057447; PMID:3194193

A, Accession: S01944

A;Molecule type: DNA A;Residues: 1-41 <COH> A;Cross-references: EMBL:X12971; NID:g53138; PIDN:CAA31414.1; PID:g53139 C;Comment: In mammals, this form is found in fetal and regenerating skeletal muscle, fet C;Genetics:

Ajfitrons: 41/3; 51/1; 101/1; 159/1; 185/1 C;Superfamily: calmodulin; calmodulin repeat homology C;Reywords: calcium binding; cardiac muscle; duplication; EF hand; heart; muscle contrac F;47-81/Domain: calmodulin repeat homology <EF1> F;126-158/Domain: calmodulin repeat homology <EF3> F;161-193/Domain: calmodulin repeat homology <EF3>

57.9%; Score 44; DB 1; Length 193; 71.4%; Pred. No. 4; tive 1; Mismatches 3; Indels

Gaps ö Query Match
Best Local Similarity 71.4'
Matches 10; Conservative

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2 KPKFEAYKAAAPA 15 g ઠ

hypothetical protein [imported] - Sinorhizobium meliloti (strain 1021) magaplasmid pSymB C;Species: Sinorhizobium meliloti C;Species: 24-Aug-2001 #sequence_revision 24-Aug-2001 #text_change 09-Jul-2004

C;Accession: G96014
R;Finan, T.M.; Weidner, S.; Wong, K.; Buhrmester, J.; Chain, P.; Vorholter, F.J.; Hernan Proc. Natl. Acad. Sci. U.S.A. 98, 9889-9894, 2001
A;Title: The complete sequence of the 1,683-4k pSymB megaplasmid from the N2-fixing endo A;Reference number: A95842; MUID:21396508; PMID:11481431 A; Accession: G96014

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A;Cross-references: UNIPROT:Q9JTQ0; GB:AL162756; GB:AL157959; NID:g7380091; PIDN:CAB8491(
A;Experimental source: serogroup A, strain 22491
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               hypothetical protein CC0674 [imported] - Caulobacter crescentus
Cippedes: Caulobacter crescentus
Cippedes: Caulobacter crescentus
Cipaces 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 09-Jul-2004
Cipacession: G87332
Rivibrana, W.C.; Feldblyuw, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, J.El
B.; Laub, M.T.; DeBoy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Kolon
n, J.; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M.
Proc. Natl. Acad. Sci. US.A. 98, 4136-411, 2001
Proc. Natl. Acad. Sci. US.A. 99, 4136-411, 2001
A; Fitle: Complete Genome Sequence of Caulobacter crescentus.
A; Reference number: A87249; MUID:21173698; PMID:11259647
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NiAlternate names: ACC oxidase
C;Species: Sorghum bicolor (sorghum)
C;Dacession: T14643
R;Finlayson, S.A; Lee, I.J; Mullet, J.E.; Morgan, P.W.
Plant physiol, 119, 1083-1199;
A;Fille: The mechanism of rhythmic ethylene production in sorghum. The role of phytochrom A;Reference number: Z18166; MUID:99169299; PMID:10069847
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Accession: T14643
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Status: preliminary;
A;Molecule type: mRNA
A;Residues: 1-316 <FIN>
A;Residues: 1-316 <FIN>
A;Cross-references: UNIPROT:O81606; EMBL:AF079588; NID:g3386564; PIDN:AAC28488.1; PID:g3: C;Genetics:
A;Genetics:
C;Function:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A,Cross-references: UNIPROT:Q9AAC8; GB:AE005673; NID:g13421893; PIDN:AAK22659.1; GSPDB:GR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Description: catalyzes the reaction of 1-aminocyclopropane-1-carboxylic acid, oxygen ar
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -aminocyclopropane-1-carboxylate oxidase (EC 1.4.3.-) ACO1 [similarity] - sorghum
                                                                                                                                                                                                                                                                                                                                                     ö
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                                                                                                                                                                                                                                                                                   Length 336;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 2; Length 389;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
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C; Superfamily: 1-aminocyclopropane-1-carboxylate oxidase
C; Keywords: ethylene biosynthesis; oxidoreductase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4;
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                                                                                                                                                                                                                                                                                   5
                                                                                                                                                                                                                                                                               56.6%; Score 43; DB 53.3%; Pred. No. 10;
                                                                                                                                                                                                                                                                                                                                                 2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1; Mismatches
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Pred. No. 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 43;
Pred. No.
                                                                                                                                       A;Gene: trpS; NMA1682
C;Superfamily: tryptophan-tRNA ligase
C;Keywords: ligase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        56.6%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  243 ESPLFEIYKAFSTPS 257
                                                                                                                                                                                                                                                                                                                                                                                                                    1 EKPKFEAYKAAAAPA 15
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                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
Matches 8; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity
Matches 9; Conserv
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                 A;Residues: 1-336 <PAR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -389 <STO>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Accession: G87332
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C;Genetics:
A;Gene: CC0674
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A:Status: preliminary
A:Molecule type: DNA
A:Cross-references: UNIPROT:092TW2; GB:AL591985; PIDN:CAC49783.1; PID:g15141270; GSPDB:G
A:Experimental source: strain 1021, megaplasmid pSymB
A:Galibert, F.; Finan, T.W.; Long, S.R.; Puhler, A.; Abola, P.; Ampe, F.; Barloy-Hubler, pela, D.; Chain, P.; Cowie, A.; Davis, R.W.; Dreano, S.; Federspiel, N.A.; Fisher, R.F.; L.; Hyman, R.W.; Jones, T.
A:Hyman, R.W.; Jones, T.
A:Authors: Kahn, M.L.; Kalman, S.; Keating, D.H.; Kiss, E.; Komp, C.; Lelaure, hebault, P.; Vandenbol, M.; Vorholter, F.J.; Weidner, S.; Wells, D.H.; Wong, K.; Yeh, K. A;Title: The composite genome of the legume symbiont Sinorhizobium meliloti.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Lryptophanyl-tRNA synthetase NMB1471 [imported] - Neisseria meningitidis (strain MC58 se CiSpecies: Neisseria meningitidis
CiSpecies: Neisseria meningitidis
CiSpecies: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 09-Jul-2004
CiAccession: B81081
R;Tettelin, H.; Saunders, N.J.; Heidelberg, J.; Jeffries, A.C.; Nelson, K.E.; Eisen, J.A. Hickey, B.K.; Haft, D.H.; Salzberg, S.L.; White, O.; Fleischmann, R.D.; Dougherty, B.A.; ri, H.; Qin, H.; Vamathevan, J.; Gill, J.; Scarlato, V.; Masignani, V.; Pizza, M. Science 287, 1809-1815, 2000
A;Authors: Grandi, G.; Sun, L.; Smith, H.O.; Fraser, C.M.; Moxon, E.R.; Rappuoli, R.; Ve A;Tutle: Complete genome sequence of Neisseria meningitidis serogroup B strain MC58.
A;Reference number: A81000; MUID:20175755; PMID:10710307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A,Cross-references: UNIPROT:09JY09, GB:AE002496; GB:AE002098; NID:g7226701; PIDN:AAF4182
A,Experimental source: serogroup B, strain MC58
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R; Parkhill, J.; Achtman, M.; James, K.D.; Bentley, S.D.; Churcher, C.; Klee, S.R.; Morel ; Holzoyd, S.; Jagels, K.; Leather, S.; Moule, S.; Mungall, K.; Quail, M.A.; Rajandream, Nature 404, 502-506, 2000
A; Title: Complete DNA sequence of a serogroup A strain of Neisseria menigitidis 22491.
A; Reference number: A81775; MUID: 20222556; PMID: 10761919
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          tryptophan-tRNA ligase (EC 6.1.1.2) NMA1682 [imported] - Neisseria meningitidis (strain C.Specdes) Neisseria meningitidis (5.Specdes) Neisseria meningitidis C.Date: 05-May-2000 #sequence_revision 05-May-2000 #text_change 09-Jul-2004 C.Accession: B81863
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Pred. No. 9.5;
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ed. No. 9.5; Mismatches

2,

Conservative KPKFEAYKAAAAPA

Local Similarity les 8; Conserv

A;Contents: annotation C;Genetics: A;Gene: SMD20676

A; Genome: plasmid Query Match 12

:[: ||:::||||| RPQPEAFESAAAPA 79

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56.6%; 57.1%;

5,

56.6%; Score 43; DB 53.3%; Pred. No. 10; tive 2; Mismatches

Best Local Similarity 53.3 Matches 8; Conservative

Query Match

ESPLFEIYKAFSTPS 257 1 EKPKFEAYKAAAPA 15

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A; Accession: E81863 A; Status: preliminary A; Molecule type: DNA

A,Gene: NMB1471 C,Superfamily: tryptophan-tRNA ligase

A, Molecule type: DNA A, Residues: 1-336 <TET>

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A;Molecule type: mRNA
A;Residues: 1.554 cCHE>
A;Residues: 1.554 cCHE>
A;Residues: 1.554 cCHE>
A;Cross-references: UNIPROT:Q39760; EMBL:U23205; NID:g1045313; PIDN:AAA93065.1; PID:g104
A;Experimental source: cultivar Nanking
C;Superfamily: vetispiradiene synthase 1
C;Keywords: phytoalexin biosynthesis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    myosin alkali light chain 4, embryonic - chicken
MyAlternate names: myosin Li23 catalytic light chain
C;Alternate names: myosin Li23 catalytic light chain
C;Species: Gallus gallus (chicken)
C;Date: 01-Dec-1989 #sequence_revision 03-Oct-1995 #text_change 09-Jul-2004
C;Accession: 802065; A29473
R;Nabeshima, Y I.; Nabeshima, Y I.; Kawashima, M.; Nakamura, S.; Nonomura, Y.; Fujii-Kuriy J. Mol. Biol. 204, 497-505, 1988
A;Title: Isolation of the chick myosin alkali light chain gene expressed in embryonic gi A;Accession: 802065; MUID:89141751; PMID:3225843
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Molecule type: DNA
A;Residues: 1-185 <NAB>
A;Residues: 1-185 <NAB>
A;Residues: 1-185 <NAB>
A;Cross-references: UNIPROT:P09540; EMBL:X14428
A;Cross-references: UNIPROT:P09540; EMBL:X14428
A;Mote: the authors translated the codon CGG for residue 71 as Ala
B;Kawashima, M.; Nabeshima, Y.; Obinata, T.; Fujii-Kuriyama, Y.
A;Title: A common myosin 1ight chain is expressed in chicken embryonic skeletal, cardiac
A;Reference number: A29473; MUID:88032983; PMID:3667580
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Molecule type: mRNA
A;Residues: 1-93,'L',95-165,'L',167-185 <KAW>
A;Cross references: GB:U02823; NID:g212339; PID:AAA48957.1; PID:g212340
A;Cros: the authors translated the codon CTG for residue 94 as Met and TAC for residue 1
C;Comment: In chicken, this form is transiently expressed in embryonic skeletal, cardiac
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Introns: 33/3; 43/1; 93/1; 151/1; 177/1
C; Complex: The myosin molecule contains two heavy chains, two alkali light chains, and t
C; Superfamily: calmodulin; calmodulin repeat homology
C; Keywords: brain; calcium binding; duplication; EF hand; muscle contraction
E; 39-73/Domain: calmodulin repeat homology <EE1.>
F; 118-150/Domain: calmodulin repeat homology <EF3.>
F; 153-185/Domain: calmodulin repeat homology <EF3.>
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Nucleic Acids Res. 18, 1581-1586, 1990
A;Title: Complete cDNA sequence of rat atrial myosin light chain 1: patterns of expressi A;Reference number: S09236; MUID:90221887; PMID:2326197
A;Accession: S09236
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N'Alternate names: MLC1A; MLC1emb; myosin L1 catalytic light chain, atrial
C;Species: Rattus norvegicus (Norway rat)
C;Date: 29-Jan-11993 #sequence_revision 03-Oct-1995 #text_change 09-Jul-2004
                                                                                                                                                                                                                     Length 554;
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25;
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                                                                                                                                                                                                                     Score 42;
Pred. No.
                                                                                                                                                                                                               55.3%;
ilarity 61.5%;
Conservative 1
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                                                                                                                                                                                                                                                                                                                                           2 KPKFEAYKAAAAP 14
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les 8; Conserv
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nes 9; Conserv
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Matches
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                                                                                                                                                                                                                                                               trar protein homolog - Sphingomonas aromaticivorans plasmid pNL1
C;Species: Sphingomonas aromaticivorans
C;Species: Sphingomonas aromaticivorans
C;Species: Sphingomonas aromaticivorans
C;Date: 11-Jan-2000 #sequence_revision 11-Jan-2000 #text_change 09-Jul-2004
C;Accession: T31225
R;Romine, M.F.; Stillwell, L.C.; Wong, K.K.; Thurston, S.J.; Sisk, E.C.; Sensen, C.W.; G #submitted to the EMBL Data Library, July 1998
A;Recription: Complete sequence of a 184 kb catabolic plasmid from Sphingomonas aromatians A;Reference number: 220992
A;Accession: T31225
A;Accession: T31225
A;Accession: T31225
A;Residues: 1-270 «ROM»
A;Residues: 1-270 «ROM»
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Cross-references: UNIPROT:085933; EMBL:AF079317; NID:g3378261; PID:g3378366; PIDN:AADG
C;Genetics:
A;Genome: plasmid pNL1
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A;Residues: 1-554 <CHE>
A;Crose-references: UNIDROT:039761; EMBL:U23206; NID:g1045311; PIDN:AAA93064.1; PID:g104
A;Experianal source: cultivar Nanking
C;Superfamily: vetispiradiene synthase 1
C;Keywords: phytoalexin biosynthesis
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C;Species: Gossypium arboreum
C;Species: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 09-Jul-2004
C;Accession: S68366
R;Chen, X.Y.; Chen, Y.; Heinstein, P.; Davisson, V.J.
Arch Biochem. Biophys. 324, 255-266, 1995
A;Fitle: Cloning, expression, and characterization of (+)-delta-cadinene synthase:
A;Reference number: S68365; MUID:96132653; PMID:8554317
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      Indels
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Pred. No. 12;
0; Mismatches
   Mismatches
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1; Mismatches
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                                                                                            ::|:|| |||| :||
298 KEPRFEAVKAAAPKSSPA 315
   4
                                                         1 EKPKFEAYKAAA---APA 15
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76.9%;
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394 KPSFEEFKANALP 406
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Best Local Similarity 76.9
Matches 10; Conservative
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52.6%;
                                                                                                                 180 EKPKEHAYKAQEA 192
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Best Local Similarity 52.64
Matches 10; Conservative
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             9; Conservative
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hes 10; Conserv
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A;Gene: CESP:F17C11.9
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A;Residues: 1-193 <ROV>
A;COSB-references: UNIPROT:P17209; EMBL:X51531; NID:g57512; PIDN:CAA35911.1; PID:g57513
A;Cross-references: UNIPROT:P17209; EMBL:X51531; NID:g57512; PIDN:CAA35911.1; PID:g57513
C;Comment: In mammals, this form is found in fetal and regenerating skeletal muscle, fet
C;Superfamily: calmodulin; calmodulin repeat homology
C;Keywords: calcium binding; cardiac muscle; duplication; EF hand; heart; muscle contract
F;47-81,Domain: calmodulin repeat homology <EF3>
F;126-158/Domain: calmodulin repeat homology <EF3>
F;161-193/Domain: calmodulin repeat homology <EF4>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1-aminocyclopropane-1-carboxylate oxidase (EC 1.4.3.-) ACO2 - sorghum (fragment)
N;Alternate names: ACC oxidase
C;Species: Sorghum bicolor (sorghum)
C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 09-Jul-2004
C;Accession: T14644
R;Finlayson, S.A.; Lee, I.J.; Mullet, J.E.; Morgan, P.W.
R;Finlayson, S.A.; Lee, I.J.; Mullet, J.E.; Morgan, P.W.
A;Title: The mechanism of rhythmic ethylene production in sorghum. The role of phytochrc A;Reference number: Z18166; MulD:99169299; PMID:100669847
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148130
hypothetical protein T4C9.40 - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 20.Apr-21000 #sequence_revision 20.Apr-2000 #text_change 09-Jul-2004
C;Accession: T48130
R;Bevan, M.; Peters, S.A.; van Staveren, M.; Dirkse, W.; Stiekema, W.; Bancroft, I.; Mew Bubmitted to the Protein Sequence Database, June 1999
A;Reference number: Z24485
A;Accession: T48130
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                                                                                                                                                                                                                                               Query Match 53.9%; Score 41; DB 1; Length 193; Best Local Similarity 64.3%; Pred. No. 13; Matches 9; Conservative 1; Mismatches 4; Indels
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C;Superfamily: 1-aminocyclopropane-1-carboxylate oxidase
C;Keywords: ethylene biosynthesis; oxidoreductase
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A;Experimental source: cultivar Columbia; BAC clone T4C9
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A;Molecule type: mRNA
A;Residues: 1-194 <FIN>
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Pred. No. 13;
4; Mismatches
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Matches 8; Conservative
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A;Molecule type: DNA
A;Residues: 1-200 <BEV>
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A,Introns: 132/1
A,Note: T4C9.40
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Ribelvecchio, V.G.; Kapatral, V.; Redkar, R.J.; Patra, G.; Mujer, C.; Los, T.; Ivanova, P.; Maurr, M.; Golteman, B.; Selkov, B.; Barzer, P.H.; Hagius, S.; O'Callaghan, D.; Letessc Proc. Natl. Acad. Sci. U.S.A. 99, 443-448, 2000.
A;Title: The genome sequence of the facultative intracellular pathogen Brucella melitens: A;Reference number: AD3252; PMID:11756688
A;Accession: AG3508
A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                      A;Cross-references: UNIPROT:Q8YE25; GB:AE008917; PIDN:AAL53234.1; PID:g17984111; GSPDB:GNA;Experimental source: strain 16M
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                              C;Species: Brucella melitensis
C;Date: 01-Feb-2002 #sequence_revision 01-Feb-2002 #text_change 09-Jul-2004
C;Accession: AG3508
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Cippedies: Caenorhabditis elegans
Cipate: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
Cipacession: T21061
Rimchurray, A.
Submitted to the EMBL Data Library, May 1996
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ransporter BMEI2053 [imported] - Brucella melitensis (strain 16M)
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C;Superfamily: translation elongation factor eEF-1 gamma chain
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A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-398 cMLb.
A;Cross-references: UNIPROT:P54412; EMBL:Z72507; PII
A;Experimental source: clone F17C11
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01-007-1996 (Rel. 34, Created)
01-007-1996 (Rel. 34, Created)
01-N0V-1997 (Rel. 35, Last sequence update)
01-N0V-2095 (Rel. 46, Last annotation update)
00S ribosomal protein L22.
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                                                     March 31, 2005, 02:18:02 ; Search time 80.5645 Seconds (without alignments) 95.342 Million cell updates/sec
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Copyright (c) 1993 - 2005 Compugen Ltd.
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RL22_DROME
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Q7UTK6
Q69YQ8
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Q7NVT5
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GENDL; ABO17333; AAU40801.1; -. EMBL; CP0000002; AAU23441.1; -. SEQUENCE 781 AA, 86477 MW; 634995AC2DA5D3D8 CRC64;
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Rey M.W., Ramalya P., Nelson B.A., Brody-Karpin S.D., Zaretsky E.J., Tang M., de Leon A.L., Xiang H., Gusti V., Clausen I.G., Olsen P.B., Rasmussen M.D., Andersen J.T., Jorgensen P.L., Larsen T.S., Sorokin A., Bolotin A., Lapidus A., Galleron N., Ehrlich S.D., Berka R.M.;
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"The Complete Genome Sequence of Bacillus licheniformis DSM13, Organism with Great Industrial Potential.";

J. Mol. Microbiol. Biotechnol. 7:204-211(2004).
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25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
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Name=spoIIIE; ORFNames=BL01204, BLi01906;
Bacillus licheniformis DSM 13.
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QBFRIS
QBKG95
MLEF_CHICK
MLEF_RAT
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EKPEVQAYEAPAAPA 278
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les 10; Conservative
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\begin{matrix} \mathbf{u}_{1} & \mathbf{u}_{2} & \mathbf{u}_{3} & \mathbf{u}_{2} & \mathbf{u}_{3} & \mathbf{u}_{3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PubMed=15383718;
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299 AA

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DOMAIN
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RXATRANDEMERGRALBY;
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RX AMENDATION CALINKER S.E., Holt R.A., Evans C.A., Gocarne J.D.;
RA Amenatides R.A., Lewis S.E., Holt R.A., Evans C.A., Gocarne J.D.;
RA Amenatides R.A., Lewis S.E., Holt R.A., Exhance R.A., Galle R.F.,
RA GEOTGE R.A., Lewis S.E., Michards R.A., Galle R.B.,
RA Brandon R.C., Rogers Y.-H.C., Blazel R.G., Champe M., Pfeiffer B.D.,
RA Ballew R.M., Basu A., Baxer E.G., Helf G., Nelson C.R., Miklos G.L.G.,
RA Ballew R.M., Basu A., Baxendale U., Bayraktaroglu L., Beasley E.M.,
RA Ballew R.M., Basu A., Baxendale U., Bayraktaroglu L., Beasley E.M.,
RA Ballew R.M., Bouck J.E., Downes M., Dughakov S.,
RA Gorova D., Botcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferriera S., Punkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferriera S., Punkov B.C., Dunn P.,
RA Glodek A., Gong F., Gorrell J.H., Gul Z., Galbart W.M., Glasser K.,
RA Houston K.A., Howlann T.J., Wal M.-H., Dlegasor K.,
Alandh B., Kodirac C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
Lasko P., Lei Y., Levitsky A.A., Li J.H., Li Z., Lidang Y., Lin X.,
Lasko P., Lei Y., Levitsky A.A., Li J.H., Li Z., Lidang Y., Lin X.,
Randel B.E., Kodirac C.D., Kraft C., Kravitz S., Molperson D.L.,
Ranch C.M., Moyn W. Murphy L., Murzhy D.M., Nelson D.L.,
Ranch C.M., Palanca C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
Ranch C., Siden-Kiamos I., Sambson M., Stupski M.P., Smith T.,
Spier E., Spradling A.C., Stapleton M., Stupski M.P., Waissenbach J.,
Ryinkas R., Tector C., Turner R., Vonter E., Wang A.H., Wang Z.-Y., Wasserman D.A., Wainstock G.M., Waissenbach J.,
Wang Z.-Y., Wassarman D.A., Weilsholds R., Zhong R.N., Zhong F.N., Zhong F.N., Zhong Y., Zhu S., Zhu X., Zhu S., Zhu X., Zhu S., Zhu X., Zhu S., 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=20196011; PubMed=10731137; DOI=10.1126/science.287.5461.2220; Benos P.V., Gatt M.K., Ashburner M., Murphy L., Harris D., Barrell B.G., Ferraz C., Vidal S., Brun C., Demailles J., Cadieu E., Dreano S., Gloux S., Lelaure V., Mottier S., Galibert F., Borkova D., Minana B., Kafatos F.C., Louis C., Siden-Kiamos I., Bolshakov S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENOME REANNOTATION.
MEDINE=22480669; PubMed=12537572;
MISTAR S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,
Hradecky, P., Huang Y., Kaminker J.S., Millburn G.H., Prochnik S.B.,
Smith C.D., Tupy J.L., Whitfield B.J., Bayraktaroglu L., Berman B.P.
Bettencourt B.R., Celniker S.E., de Grey A.D.N.J., Drysdale R.A.,
Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q.,
Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Annotation of the Drosophila melanogaster euchromatic genome:
                           Drosophila melanogaster (Fruit fly).
Bukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                           Glover C.V.C., Bidwai A.P., Zhao W.F.;
Submitted (OCT-1996) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Genome Biol. 3:RESEARCH0083.1-RESEARCH0083.22(2002).
  Name=RpL22; ORFNames=CG7434;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                systematic review.";
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                                                                                                                                 NCBI_TaxID=7227;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
Papagiannakis G., Spanos L., Cox S., Madueno E., de Pablos B., Modolell J., Peter A., Schoettler P., Werner M., Mourkioti F., Beinert N., Dowe G., Schaefer U., Jaeckle H., Bucheton A., Callister D.M., Campbell L.A., Darlamitsou A., Henderson N.S., McMillan P.J., Salles C., Tait E.A., Valenti P., Saunders R.D.C., Glover D.M.;
                                                                                                                                                                                   "From sequence to chromosome: the tip of the X chromosome of D.
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01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAY-2000 (TrEMBLrel. 24, Last sequence update)
01-UDN-2003 (TrEMBLrel. 24, Last annotation update)
Ribosomal protein L22 (Fragment).
Name-ERPL2; Synonyms=rpl2;
Drosophila melanogaster (Fruit fly).
Bukaryota; Metazoa, Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                      Science 287:2220-2222(2000).
-!- SIMILARITY: Belongs to the ribosomal protein L22e family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Asp/Glu-rich (highly acidic). 46A99005610E4EB0 CRC64;
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Pred. No. 17;
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Poly-Ala.
Poly-Ala.
Poly-Ala.
Poly-Ala.
Poly-Ala.
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InterPro; IPR002671; Ribosomal L22e.
Pfam; PF01776; Ribosomal L22e; I.
ProDom; PD007306; Ribosomal L22e; I.
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EMBL; AF080131; AAD19341.1; -.

FlyBases; FBgm0015289; RpL22,

GO; GO:0005622; C:intracellular; IEA.

GO; GO:0005840; C:ribosome; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 73.33
Matches 11, Conservative
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50
70
1112
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299
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                                                                                                                                                                                                                 melanogaster.";
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S T X X Y Y S

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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo. NCBI_TaxID=9606;
                                                                                                                                                                            Gloeckner F.O., Kube M., Bauer M., Teeling H., Lombardot T.,
Ludwig W., Gade D., Beck A., Borzym K., Heitmann K., Rabus R.,
Schlesner H., Amann R., Reinhardt E.,
"Complete genome sequence of the marine planctomycete Pirellula
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.

TISSUE=Skeletal muscle;
The German cDNA Consortium;
The German cDNA consortium;
Fobo G., Han M., Wiemann S.;
Submitted (JUL-2004) to the EMBL/GenBank/DDBJ databases.
Hypothetical protein.
NON TER 1340 1340 13572 MW; FA4635BB5BE64394 CRC64;
                                                                                                                                   STRAIN=1;
MEDLINE=22735913; PubMed=12835416; DOI=10.1073/pnas.1431443100;
                    Bacteria; Planctomycetes; Planctomycetacia; Planctomycetales;
Planctomycetaceae; Pirellula.
                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 45; DB 2; Length 800;
Pred. No. 63;
                                                                                                                                                                                                                                                                                 Proc. Natl. Acad. Sci. U.S.A. 100:8298-8303(2003).

EMBL, BX294139; CAD73430.1; -
InterPro; IPR001345; PG/ABGM mutase.

PROSITE; PS00175; PG MUTASE; UNKNOWN 1.

COMDLETE PROTEOME; Hypothetical protein.

SEQUENCE 800 AA; 91385 MW; C32C861687CDB466 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       25-OCT-2004 (TrEMBLrel. 28, Created)
25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
Hypothetical protein DKFZp4511127 (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             069YQ9 PRELIMINARY; PRT; 1614 AA.
069YQ9;
25-OCT-2004 (TrEMBLrel. 28, Created)
25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
Hypothetical protein DKFZp451A076 (Fragment).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  57.18;
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634 ENEEFEAYSPAAAP 647
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      8; Conservative
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      Rhodopirellula baltica.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sest Local Similarity
                                                                                                              SEQUENCE FROM N.A.
                                                                      NCBI_TaxID=117;
                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
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                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Nature 0:0-0(2003).
-!- CAUTION: The sequence shown here is derived from an EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is preliminary data.
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Bukaryota, Fungi, Ascomycota, Pezizomycotina, Sordariomycetes,
Sordariomycetidae, Sordariales, Sordariaceae, Neurospora.
GO, GO:0003735; F:structural constituent of ribosome; IEA. 60; GO:0006412; F:sprotein biosynthesis; IEA. InterPro; IPR003571; Fibosomal L22e. Pfam; PF01776; Ribosomal L22e; 1.
                                                                                                                                                                            2; Length 312;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             60.5%; Score 46; DB 2; Length 458; 66.7%; Pred. No. 25;
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                                                                                                                                                                                                                       4; Indels
                                                                                                                          312 AA; 32273 MW; 0BE9A15CB473083B CRC64;
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SEQUENCE 458 AA; 49949 MW; 196D609EF9320496 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Last sequence update)
Last annotation update)
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Last annotation update)
                                                                                                                                                         60.5%; Sco...
73.3%; Pred. No. ...
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-MAR.2004 (TrEMBLrel. 26, 01-MAR.2004 (TrEMBLrel. 26, 01-MAR.2004 (TrEMBLrel. 26, Predicted protein. Name=NCU03083.1;
                                                                                                                                                                                                                                                               1 EKPKFEAYKAAAPA 15
                                                                                                                                                                                                                                                                                                        49 ЕКРКАЕААКРАААА 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 EKPKFEAYKAAAPA 15
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                                                                                                                                                                                                                  11; Conservative
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OrderedLocusNames=RB3828;
                                                                                                                                                                                                                                                                                                                                                                                                                  PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRELIMINARY;
                                                                                                                                                                         Query Match
Best Local Similarity
Matches 11; Conserva
                                                                                   Ribosomal protein.
NON TER 1
SEQUENCE 312 AA;
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O7UTK6 ID 07 AC 07 DT 01 DT 01 DD 01 GN 01

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Length 1340;

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Gaps

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3; Indels

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Length 192;

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SEQUENCE Query Match Matches

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Submitted (FEB-1996) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Musa acuminata (Banana).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Lilliopsida; Zingiberales; Musaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-0CT-2003 (TrEMBLrel. 25, Created)
01-0CT-2003 (TrEMBLrel. 25, Last sequence update)
01-0AR-2004 (TrEMBLrel. 26, Last annotation update)
Probable GTP-binding protein.
OrderediocusNames-BP0747;
Bordetella pertussis.
Bacteria, Proteobacteria, Betaproteobacteria, Burkholderiales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  57.9%; Score 44; DB 2; Length 315; 57.1%; Pred. No. 38; 1.1% 3; Mismatches 3; Indels
                                                                                                                                                                                                                                                  192 AA; 21028 MW; B0439D512FA19C38 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-MAY-1997 (TrEMBLrel. 03, Last sequence update) 01-JUN-2002 (TrEMBLrel. 21, Last annotation update) 1-aminocyclopropane-1-carboxylate oxidase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HSSP, Q96323; IGP6.
GO; GO:0016491; F:oxidoreductase activity; IEA.
InterPro: IFR005123; 2OG-FeII_Oxy.
IFRam; PF03171; 2OG-FeII_Oxy; I.
Iron; Oxidoreductase.
                                                                                                                                                                                                                                                                                        Score 44; DB 1; Pred. No. 24; 1; Mismatches
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                                                                                                                        MGD; MGI:97267; Myla.
InterPro; IPR002048; EF-hand.
InterPro; IPR010983; EF Hand like.
Probom; PD000012; EF-hand; 2.
Multigene family; Muscle protein; Myosin.
INT MET
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                       EMBL; M20771; AAA39721.1; JOINED.
EMBL; X12971; CAA31414.1; -.
EMBL; M19436; AAA39720.1; -.
PIR; A31114; MOMS4E.
HSSP; P02607; 1BR1.
                                                                                                                                                                                                                                                                                             57.9%;
71.4%;
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les 8; Conservative
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298 KEPRFEAMKATALP 311
                                                                                                                                                                                                                                                                                                                                                                           2 KPKFEAYKAAAPA 15
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                                                                                                                                                                                                                                                                                                           Local Similarity 71.4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Name=bacol;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    family
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Q7VZX6;
      EMBL;
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EMBL;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=88315068; PubMed=2842339;
Barton P.J.R., Robert B., Cohen A., Garner I., Sassoon D., Weydert A.,
Buckingham M.E.;
                                                                                                                                                                                                                                                                                                                                                      Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Promoter analysis of myosin alkali light chain genes expressed in mouse striated muscle.";
Nucleic Acids Res. 16:10037-10052(1988).
-!- SUBUNIT: Myosin is an hexamer of 2 heavy chains and 4 light
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
NCBI TaxID=10090;
                                                                                               TISSUE-Skeletal muscle;
The German cDNA Consortium;
Koehrer K., Beyer A., Messe H.W., Weil B., Amid C., Osanger A.,
Fobo G., Han M., Wiemann S.;
Submitted (JUL-2004) to the EMBL/GenBank/DDBJ databases.
EMBL, AL832347, CAH10406.1; -.
Hypothetical protein.
NON_TER 1614 1614
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Structure and sequence of the myosin alkali light chain gene expressed in adult cardiac atria and fetal striated muscle."; J. Biol. Chem. 263:12669-12676(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             109541;
01-MAR-1989 (Rel. 10, Created)
01-FEB-1991 (Rel. 17, Last sequence update)
05-JUL.2004 (Rel. 44, Last annotation update)
Myosin light chain 1, atrial/fetal isoform (MLCIA) (MLCIEMB).
                                                                                                                                                                                                                                                                                                       59.2%; Score 45; DB 2; Length 1614; 64.3%; Pred. No. 1.2e+02; ive 1; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=89057447; PubMed=3194193;
Cohen A., Barton P.J.R., Robert B., Garner I., Alonso S.,
Buckingham M.E.;
                                                                                                                                                                                                                                                                 1614 AA; 175041 MW; FCE219C927BAEB9B CRC64;
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EMBL; M31017; AAA39721.1; JOINED.
EMBL; M20769; AAA39721.1; JOINED.
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562 ENERFEAYSPAAAP 575
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                                                                                                                                                                                                                                                                                                                          Local Similarity 64.3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STANDARD;
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                                                                              SEQUENCE FROM N.A.
                                 NCBI_TaxID=9606;
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ID MLEF_MOUSE
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Gaps

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Alcaligenaceae; Bordetella.

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Q7WQL8
ID Q7WQL8
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Q92TW2
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                                         STRAIN=Tohama I / ATCC BAA-589 / NCTC 13251;

MEDLINE=22827954; PubMed=12910271; DOI=10.1038/ng1227;

MEDLINE=22827954; PubMed=12910271; DOI=10.1038/ng1227;

MARTIS D.E., Holden M.T.G., Churcher C.M., Bentley S.D., Mungall K.L.,

Harris D.E., Holden M.T.G., Churcher C.M., Bantley S.D., Mungall K.L.,

Cardeno-Tarraga A.-M., Temple L., James K.D., Harris B., Quail M.A.,

A Achtman M., Atkin R., Basker S., Basham D., Bason N., Cherevach I.,

Chillingworth T., Collins M., Cronin A., Davis P., Doggett J.,

Reltwell T., Goble A., Hamlin N., Hauser H., Holroyd S., Jagels K.,

Leather S., Moule S., Norberczak H., O'Neil S., Ormond D., Price C.,

Rabbinowitsch E., Rutter S., Sanders M., Sauders D., Seeger K.,

Sharp S., Simmonds M., Skelton J., Squares R., Squares S., Stevens K.,

Unwin L., Whitehead S., Barrell B.G., Maskell D.J.,

"Comparative analysis of the genome sequences of Bordetella pertussis,

"The Mordetella parapertussis and Bordetella bronchiseptica.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=22827954; PubMed=12910271; DOI=10.1038/ng1227;
Parkhill J., Sebaihia M., Preston A., Murphy L.D., Thomson N.R.,
Parkhill J., Sebaihia M., Preston A., Murphy L.D., Thomson N.R.,
Parkhill J., Sebaihia M., Churcher C. M., Bentley S.D., Mungall K.L.,
Cerdeno-Tarraga A.-M., Temple L., James K.D., Harris B., Quail M.A.,
Achtman M., Akkin R., Baker S., Basham D., Bason N., Cherevach I.,
Chillingworth T., Collins M., Cronin A., Davis P., Doggett J.,
Chillingworth T., Goble A., Hamlin N., Hauser H., Holroyd S., Jagels K.,
Leather S., Moule S., Norberczak H., O'Neil S., Ormond D., Price C.,
Rabbinowitsch E., Rutter S., Sanders M., Saunders D., Seeger K.,
Mabbinowitsch E., Rutter S., Sanders M., Squares S., Stevens K.,
Unwin L., Whitehead S., Barrell B.G., Maskell D.J.,
Bordetella parapertusesis and Bordetella bronchiseptica.";
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Alcaligenaceae, Bordetella.
NCBI_TaxID=519;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                57.9%; Score 44; DB 2; Length 377;
53.3%; Pred. No. 45;
iive 3; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                      377 AA; 40578 MW; 837173BEEA660FB1 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-OCT-2003 (TrEMBLrel. 25, Last sequence update) 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         377 AA.
                                                                                                                                                                                                                                                                                                          GO, GO: 0005525, F:GTP binding; IEA. InterPro; IPR006074; GTP1/OBG dom. InterPro; IPR006165; GTP1 OBG sub. InterPro; IPR001615; GTP1 OBG sub. Ffam; PF01018; GTP1 OBG; 1. Pfam; PF01026; MMR HSR1; 1. PROSITE; PS00905; GTP1 OBG; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GO; GO:0005525; F:GTP binding; IEA.
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                                                                                                                                                                                                                                                             Nat. Genet. 35:32-40(2003).
EMBL; BX640413; CAE41053.1; -.
HSSP; P44681; 1JAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Nat. Genet. 35:32-40(2003).
EMBL; BX640423; CAE40050.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Probable GTP-binding protein.
OrderedLocusNames=BPP0309;
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356 EDPRFDASRGGAAPA 370
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 EKPKFEAYKAAAAPA 15
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STRAIN=12822 / ATCC BAA-587
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      parapertussis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity 53.3
Matches 8; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE
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SEQUENCE FROM N.A.

STRAIN=RBSD / ATCC BAA-588;

MEDLINE=22827954; PubMed=12910271; DOI=10.1038/ng1227;

MEDLINE=22827954; PubMed=12910271; DOI=10.1038/ng1227;

MATAIN=RBSD / Arch W. Preston A., Murphy L.D., Thomson N.R.,

MATAIN T., Colling M.T.G., Churcher C.M., Bentley S.D., Mungall K.L.,

Achtman M., Atkin R., Baker S., Basham D., Bason N. Cherevach I.,

Chillingworth T., Collins M., Cronin A., Davis P., Doggett J.,

Chillingworth T., Collins M., Cronin A., Davis P., Doggett J.,

Chillingworth T., Gollins M., Cronin A., Davis P., Doggett J.,

Reltwell T., Goble A., Hamlin N., Hauser H., Holroyd S., Jagels K.,

Leather S., Moule S., Norberczak H., O'Neil S., Ormond D., Price C.,

Rabbinowitsch B., Rutter S., Sanders M., Saunders D., Seeger K.,

Sharp S., Simmonds M., Skelton J., Squares S., Stevens K.,

Unwin L., Whitehead S., Barrell B.G., Maskell D.J.;

M. "Comparative analysis of the genome sequences of Bordetella pertussis,

Bordetella parapartussis and Bordetella bronchiseptica.";
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Bacteria, Proteobacteria, Betaproteobacteria, Burkholderiales,
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                                                                                                                                                                                                                                  Length 377;
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                                                                                                                 PROSITE; PS00905; GTP1_OBG; 1.
Complete proteome.
SEQUENCE 377 AA; 40578 MW; 837173BEEA660FB1 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-OCT-2003 (TrEMBLrel. 25, Created)
01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
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45;
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                                                                                                                                                                                                                                  57.9%; Score 44; DB 53.3%; Pred. No. 45;
                                                                                                                                                                                                                                                                                       3; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
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01-DEC-2001 (TrEMBLrel. 19, Created)
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InterPro; IPR00617; GTP1/0BG dom.
InterPro; IPR006169; GTP1 OBG Bub.
InterPro; IPR002917; MMR. HSR1.
InterPro; IPR006169; GTP1_OBG_sub.
InterPro; IPR002917; MWR.HSR1.
Pfam; PF01018; GTP1_OBG; 1.
Pfam; PF01926; MMR.HSR1; 1.
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EMBL; BX640437; CAE30810.1; -.
HSSP; P44681; 1JAL.
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Pfam; PF01926; MMR HSR1; 1.
PROSITE; PS00905; GTP1 OBG; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Probable GTP-binding protein.
OrderedLocusNames=BB0312;
                                                                                                                                                                                                                                                                                                                                                                                    356 EDPRFDASRGGAAPA 370
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                                                                                                                                                                                                                                                                                                                                                   1 EKPKFEAYKAAAPA 15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Alcaligenaceae; Bordetella.
                                                                                                                                                                                                                                                                                                8; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRELIMINARY;
                                                                                                                                                                                                                                     Query Match
Best Local Similarity
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Best Local Similarity
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SEQUENCE 377 AA
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SYW NEIMB
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Finan T.M., Weidner S., Wong K., Buhrmester J., Chain P., Vorhoelter F.J., Hernandez-Lucas I., Becker A., Cowie A., Gouzy J., Golding B., Puehler A.;

"The complete sequence of the 1,683-kb pSymB megaplasmid from the N2-fixing endosymbion. Sinorhizobium meliloti.";

EMBL, ALS91985, CAC49783.1;

EMBL, ALS91985, CAC49783.1;

PIR, G96014, G96014, G96017, DUF930.

PIR, PR005273, DUF930.
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25-OCT-2004 (Rel. 45, Last annotation update)
Tryptophanyl-tRNA synthetase (EC 6.1.1.2) (Tryptophan--tRNA ligase)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN=22491 / Serogroup A / Serotype 4A;
MEDLINE=20222556; PubMed=10761919; DOI=10.1038/35006655;
Parkhill J., Achtman M., James K.D., Bentley S.D., Church C.M.,
Klee S.R., Morelli G., Basham D., Brown D., Chillingworth T.,
Davies R.M., Davis P., Devlin K., Feltwell T., Hamlin N., Holroyd &
Jagels K., Leather S., Moule S., Mungall K.L., Quail M.A.,
Rajandream M.A., Rutherford K.W., Simmonds M., Skelton J.,
Whitchead S., Spratt B.G., Barrell B.G.,
"Complete DNA sequence of a serogroup A strain of Neisseria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CATALYTIC ACTIVITY: ATP + L-tryptophan + tRNA(Trp) = AMP + diphosphate + L-tryptophanyl-tRNA(Trp).
SUBUNIT: Homodimer (By similarity).
SUBCELLULAR LOCATION: Cytoplasmic.
SIMILARITY: Belongs to the class-I aminoacyl-tRNA synthetase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=21396508; PubMed=11481431; DOI=10.1073/pnas.161294698;
                                                                                                                                                                                                                                    Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
Rhizobiaceae; Sinorhizobium/Ensifer group; Sinorhizobium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Neisseria meningitidis (serogroup A).
Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 43; DB 2; Length 306;
Pred. No. 55;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Complete proteome; Hypothetical protein; Plasmid.
SEQUENCE 306 AA; 32638 MW; 01D9CC644001E67E CRC64;
01-DEC-2001 (TrEMBLrel. 19, Last sequence update) 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
                                                                                                                                                       Rhizobium meliloti (Sinorhizobium meliloti).
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                                                                         Hypothetical protein SMb20676.
ORFNames=SMb20676;
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57.1%;
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66 RPQPEAFESAAPA 79
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STANDARD;
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NCBI_TaxID=65699;
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                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=382;
                                                                                                                                                                                               Plasmid pSymB
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between
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SYM NEIDAM
NO 09070
DT 28-FE

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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
oved. Usage by and for commercial
(See http://www.isb-sib.ch/announce/
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.

STRAIN=MC58 / Serogroup B;

STRAIN=MC58 / Serogroup B;

MEDLINE=201755; PubMed=10710307; DOI=10.1126/science.287.5459.1809;

Tettelin H., Saunders N.J., Heidelberg J.F., Jeffries A.C.,

Nelson K.E., Eisen J.A., Ketchum K.A., Hood D.W., Peden J.F.,

Dodson R.J., Nelson W.C., Gwinn M.L., DeBoy R.T., Peterson J.D.,

Hickey E.K., Haft D.H., Salzberg S.L., White O., Fleischmann R.D.,

Dougherty B.A., Mason T.M., Ciecko A., Parksey D.S., Blair B.,

Cittone H., Clark E.B., Cotton M.D., Utterback T.R., Khouri H.M.,

Gin H., Vamathevan J.J., Gill J., Scarlato V., Masignani V., Pizza M.,

Grandi G., Sun L., Smith H.O., Fraser C.M., Moxon E.R., Rappuoli R.,

Venter J.C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Complete genome sequence of Neisseria meningitidis serogroup B strain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Q9JYQ9;
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last sequence update)
25-OCT-2004 (Rel. 45, Last annotation update)
Tryptophanyl-tRNA synthetase (EC 6.1.1.2) (Tryptophan--tRNA ligase)
                                                                                                                                                     HAMAP, MF_00140; -; 1.
InterPro; IPR002305; tRNA-synt_1b.
InterPro; IPR002305; TrD_tRNA-synt_1.
InterPro; IPR002306; TrD_tRNA-synt_1.b.
PRAM, SPOO579; tRNA-synt_1.b; 1.
PRINTS; PR01039; TRNA-SYNTHTRP.
TIGRPAMS; TIGR00233; trpS; 1.
PROSITE; PS00179; AA TRNA_LIGAGE I; FALSE NEG.
Aminoacy1-tRNA synthetase; ATP-binding; Complete proteome; Ligase; Protein biosynthesis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -i - CATALYTIC ACTIVITY: ATP + L-tryptophan + tRNA(Trp) = AMP + diphosphate + L-tryptophanyl-tRNA(Trp).
-i - SUBUNIT: Homodimer (By similarity).
-i - SUBCELLULAR LOCATION: Cytoplasmic.
-i - SUMILARITY: Belongs to the class-I aminoacyl-tRNA synthetase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ;
0
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asteria, proteobacteria; Betaproteobacteria; Neisseriales;
Neisseriaceae; Neisseria.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 1; Length 336;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                   "KMSKS" region.
ATP (By similarity).
3400C34F42E34536 CRC64;
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modified and this statement is not removed. entities requires a license agreement (See Lor send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               336 AA
                                                                                                                                                                                                                                                                                                                                                                                   "HIGH" region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   60;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 43;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Name=trpS; OrderedLocusNames=NMB1471;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  37622 MW;
                                                                                    EMBL; AL162756; CAB84910.1; -. PIR; E81863; E81863.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              53.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Science 287:1809-1815(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               243 ESPLPEIYKAFSTPS 257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 EKPKFEAYKAAAAPA 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 53...
Best Conservative
B; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                             206 2
336 AA;
                                                                                                                                  HSSP; P00953; 1MAU.
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entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                   EMEL, AE002496; AAF41828.1; -.

R EMEL, AE002496; AAF41828.1; -.

R HSSP; P00953; 1MAU.

R TIGK; NMB4471; -.

R HAMAP; MF 00140; -.; 1.

R InterPro; 1PR002405; tRNA-synt_1b.

InterPro; 1PR002412; tRNA-synt_1.

R InterPro; 1PR002305; Try_tRNA-synt_1b.

R PROSTIE; PS00179; AA_TRNA-SYNTTRP.

R PROSTIE; PS00179; AA_TRNA_LID: 1.

R AMINOACY1-RRNA SYNTHEUSSE; ATPA-BINGING; COMplete protecome; Ligase; 1.

R PROSTIE; PS00179; AA_TRNA_LID: 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 56.6%; Score 43; DB 1; Length 336; Best Local Similarity 53.3%; Pred. No. 60; Matches 9; Conservative 2; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                               12 20 "HIGH" region.
203 207 "KMSKS" region.
206 206 ATP (By similarity).
336 AA; 37616 MW; OAE32C8COOB621AA CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BINDING
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Search completed: March 31, 2005, 02:41:11 Job time : 82.5645 secs

1 EKPKFEAYKAAAAPA 15 | | | | | | | : | : 243 ESPLFEIYKAFSTPS 257

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March 31, 2005, 02:17:12 ; Search time 88.7903 Seconds (without alignments) 65.338 Million cell updates/sec
 5.1.6
Compugen Ltd.
 version :
                                                          - protein search, using sw model
                                                                                                                                                                                                                          Gapop 10.0 , Gapext 0.5
GenCore
Copyright (c) 1993
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                                                                                                                                              US-10-056-583A-95
                                                                                                                                                                                                             BLOSUM62
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                                                          OM protein
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2105692 Total number of hits satisfying chosen parameters: seq length: 0 seq length: 2000000000 Minimum DB Maximum DB

2105692 seqs, 386760381 residues

Searched:

Minimum Match 0% Maximum Match 100% Listing first 45 summaries Post-processing:

geneseqp2003as:* geneseqp2003bs:* A Geneseq 16Dec04:* geneseqp1980s:* geneseqp1990s:* geneseqp2000s:* geneseqp2001s:* geneseqp2002s:* geneseqp2004s:* Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	Abp52301 HLA-DR2	302	~	6	6	Abp52296 HLA-DR2 1	6	Abp52303 HLA-DR2 r	Abp52270 HLA-DR2 r	Abp52297 HLA-DR2 r	Abp52291 HLA-DR2 r	Abp52263 HLA-DR2 r	Abp52272 HLA-DR2 1	Abp52259 HLA-DR2 r	Abp52257 HLA-DR2 r	Abp52300 HLA-DR2 r	4	Abp52299 HLA-DR2 1	Abp52253 HLA-DR2 r	Abp52251 HLA-DR2 r	Abp52239 HLA-DR2 r	Abp52290 HLA-DR2 r	Abp52261 HLA-DR2 r	Abp52244 HLA-DR2 r	Abp52292 HLA-DR2 r
SUMMARIES	Ω	ABP52301	ABP52302	ABP52271	ABP52298	ABP52294	ABP52296	ABP52295	ABP52303	ABP52270	ABP52297	ABP52291	ö	ABP52272 .	ABP52259	ABP52257	ABP52300	ABP52304	ABP52299	ABP52253	ABP52251	ABP52239	ABP52290	ABP52261	ABP52244	ABP52292
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	* Query Match Length	15	17	15	15	17	17	19	17	15	15	15	15	15	15	15	15	15	15	15	15	15	15	15	15	15
	& Query Match	100.0	92.8	91.3	91.3	91.3	91.3	91.3	88.4		81.2						72.5			•			68.1			68.1
	Score	69	64	63	63	63	63	63	61	57	26	53	53	52	51	51	20	20	49	48	48	48	47	47	47	47
	Result No.	1	73	m	4	2	9	7	80	Q	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25

Abp52269 HLA-DR2 m Abp52262 HLA-DR2 m Abp52264 HLA-DR2 m	HLA-	ADDS227/ HLA-DR2 m ADDS2280 HLA-DR2 m ADDS2254 HLA-DR2 m	HEA-	Abp52249 HLA-DR2 m Abp52305 HLA-DR2 m Abb63276 Drosophil	Ad896704 Drosophil Aay88969 Copeptide Aay82058 MHC Class Aag63198 Peptide w
ABP52269 ABP52262 ABP52264	ABP52267 ABP52236 ABP52265	ABP522777 ABP52280 ABP52254	ABP52240 ABP52241 ABP52248	ABP52249 ABP52305 ABB63276	ADS96704 AAY58969 AAY82058 AAG63198
	សលស			மமை	5222
47 68.1 47 68.1 46 66.7	0000		าตตต	ოოო	43 62.3 42 60.9 42 60.9 42 60.9
9 7 8		21 W 44 R			24444 25443 4444

ALIGNMENTS

HLA-DR2; MHC class II DR-2 molecule; demyelinating; multiple sclerosis; immune response; antiinflammatory; neuroprotective; proliferation; MHC class II protein inhibitor; demyelinating disease; inhibition; post-viral encephalomyelitis; post-vaccine demyelinating condition; Human leukocyte antigen; HLA; major histocompatibility complex; MHC; HLA-DR2 molecule binding peptide SEQ ID NO:95. Ź ABP52301 standard; peptide; 15 (first entry) 16-OCT-2002 ABP52301;

anti-tumour necrosis factor agent. WO200259143-A2. sapiens 01-AUG-2002. Synthetic. Ношо

Strominger JL, Fridkis-Hareli M; 24-JAN-2002; 2002WO-US002071. 24-JAN-2001; 2001US-0263569P. (HARD) HARVARD COLLEGE. WPI; 2002-608439/65.

ø New compositions comprising synthetic peptides in complex with a major histocompatibility complex class II HLADR2 protein, useful for treating demyelinating disease, e.g. multiple sclerosis, or post-viral encephalomyelitis.

Claim 28; Page 39; 54pp; English.

The present invention describes compositions (I) comprising a peptide with an amino acid sequence with tyrosine (Y), lysine (K), and/or valine residues. The complex of the peptide with a major histocompatibility complex (MHC) class II HLA-DR2 protein is involved in modulating an immune response. (I) has antiinflammatory and neuroprotective activities, and can be used as a MHC class II protein inhibitor. The compositions comprising the peptides are useful for treating demyelinating diseases

Gaps

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Length 17; 1; Indels

Score 64; DB 5; I Pred. No. 0.00087; 0; Mismatches 1;

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Conservative

14;

Similarity

Query Match Local Matches

Sequence 17 AA;

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1 EKAKFEAFKAAAAA 15 EKAKFEAFKAAAAPA 17

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92.8**%**; 93.3**%**;

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such as multiple sclerosis, post-viral encephalomyelitis, a post-vaccine demyelinating condition, and a side effect of administering an anti-tumour necrosis factor agents. The peptide further inhibits proliferation of autoantigen-specific HIA-DR2-restricted T cell clones. ABP52207 to ABP52305 represent peptides used in the exemplification of the present
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New compositions comprising synthetic peptides in complex with a major histocompatibility complex class II HLADR2 protein, useful for treating demyelinating disease, e.g. multiple sclerosis, or post-viral
                                                                                                                                                                                                                                                                                                                                                                       Human leukocyte antigen; HLA; major histocompatibility complex; MHC; HLA-DR2; MHC class II DR-2 molecule; demyelinating; multiple sclerosis; immune response; antiinflammatory; neuroprotective; proliferation; MHC class II protein inhibitor; demyelinating disease; inhibition; post-viral encephalomyelitis; post-vaccine demyelinating condition;
                                                                                                                                                 Gaps
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                                                                                                                     100.0%; Score 69; DB 5; Length 15; 100.0%; Pred. No. 0.00012; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                  HLA-DR2 molecule binding peptide SEQ ID NO:96.
                                                                                                                                                                                                                                                                      ABP52302 standard; peptide; 17 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                               anti-tumour necrosis factor agent
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 28; Page 39; 54pp; English
                                                                                                                          100.08; Fr.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Fridkis-Hareli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  24-JAN-2002; 2002WO-US002071.
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                                                                                                                                                                           1 EKAKFEAFKAAAAA 15
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                                                                                                                                                                                                                                                                                                                          (first entry)
                                                                                                                        Query Match 100.
Best Local Similarity 100.
Matches 15; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (HARD ) HARVARD COLLEGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2002-608439/65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          encephalomyelitis.
                                                                                               Sequence 15 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens.
                                                                                                                                                                                                                                                                                                                          16-OCT-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Synthetic.
                                                                   invention
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Human leukocyte antigen, HLA; major histocompatibility complex; MHC; HLA-DR2; MHC class II DR-2 molecule; demyelinating; multiple scletrosis; immune response; antiinflammatory; neuroprotective; proliferation; MHC class II protein inhibitor; demyelinating disease; inhibition; post-viral encephalowyelitis; post-vaccine demyelinating condition;

anti-tumour necrosis factor agent

HLA-DR2 molecule binding peptide SEQ ID NO:65.

(first entry)

16-OCT-2002

ABP52271;

ABP52271 standard; peptide; 15 AA.

ABP5227 RESULT

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with an amino acid sequence vith tyrospine (X), lysine (K), and/or valine residues. The complex of the peptide with a major histocompatibility complex (MHC) class II HLA-DR2 protein is involved in modulating an immune response. (I) has antiinflammatory and neuroprotective activities, and can be used as a MHC class II protein inhibitor. The compositions comprising the peptides are useful for treating demyelinating diseases such as multiple sclerosis, post-viral encephalomogelitie, a post-vaccine demyelinating condition, and a side effect of administering an anti-tumour necrosis factor agents. The peptide further inhibits proliferation of automatigen-specific liab-DR2-restricted T cell clones. ABPS2207 to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New compositions comprising synthetic peptides in complex with a major histocompatibility complex class II HLADR2 protein, useful for treating a demyelinating disease, e.g. multiple sclerosis, or post-viral
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ABP52305 represent peptides used in the exemplification of the present
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    present invention describes compositions (I) comprising a peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 63; DB 5; Length 15;
Pred. No. 0.0011;
2; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 28; Page 39; 54pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  91.3%;
86.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 86...
Best 13; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2002-608439/65.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                encephalomyelitis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 15 AA;
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Strominger JL, Fridkis-Hareli

(HARD) HARVARD COLLEGE

24-JAN-2002; 2002WO-US002071. 24-JAN-2001; 2001US-0263569P.

WO200259143-A2 Homo sapiens. Synthetic.

01-AUG-2002.

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Gaps

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1 EKAKFEAFKAAAAA 15

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The present invention describes compositions (1) comprising a peptide with an amino acid sequence with tyrosine (Y), lysine (K), and/or valine residues. The complex of the peptide with a major histocompatibility complex (MHC) class II HLA-DE2 protein is involved in modulating an immune response. (1) has antiinflammatory and neuroprotective activities, and can be used as a MHC class II protein inhibitor. The compositions comprising the peptides are useful for treating demyelinating diseases such as multiple sclerosis, post-viral encephalomyelitis, a post-vaccine demyelinating condition, and a side effect of administering an antitumour necrosis factor agents. The peptide further inhibits proliferation of autoantigen-specific HLA-DE2-restricted T cell clones. ABP52207 to ABP52305 represent peptides used in the exemplification of the present

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The present invention describes compositions (I) comprising a peptide with an amino acid sequence with tyrosine (Y), lysine (K), and/or valine residues. The complex of the peptide with a major histocompatibility complex (MHC) class II HIA-DE2 protein is involved in modulating an immune response. (I) has antiinflammatory and neuroprotective activities, and can be used as a MHC class II protein inhibitor. The compositions comprising the peptides are useful for treating demyelinating diseases such as multiple sclerosis, post-viral encephalomyelitis, a post-vaccine demyelinating condition, and a side effect of administering an antituour necrosis factor agents. The peptide further inhibits proliferation of autoantigen-specific HIA-DE2-restricted T cell clones. ABBF52307 to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New compositions comprising synthetic peptides in complex with a major histocompatibility complex class II HLADR2 protein, useful for treating demyelinating disease, e.g. multiple sclerosis, or post-viral encephalomyelitis.
                                                                                                                                     Human leukocyte antigen; HLA; major histocompatibility complex; MHC; HLA-DR2; MHC class II DR-2 molecule; demyelinating; multiple sclerosis; immune response; antiinflammatory; neuropprotective; proliferation; MHC class II protein inhibitor; demyelinating disease; inhibition; post-viral encephalomyelitis; post-vaccine demyelinating condition;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 63; DB 5; Length 15;
Pred. No. 0.0011;
2; Mismatches 0; Indels
                                                                                                    HLA-DR2 molecule binding peptide SEQ ID NO:92.
ABP52298 standard; peptide; 15 AA.
                                                                                                                                                                                                                               anti-tumour necrosis factor agent
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86.7%;
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EKAKYEAYKAAAAA 15
                                                                   (first entry)
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                                                                                                                                                                                                                                                                  sapiens.
                                                                   16-OCT-2002
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Best Local (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New compositions comprising synthetic peptides in complex with a major histocompatibility complex class II HLADR2 protein, useful for treating a demyelinating disease, e.g. multiple sclerosis, or post-viral encephalomyelitis.
                                                                                                                    Human leukocyte antigen; HLA; major histocompatibility complex; MHC; HLA-DR2; MHC class II DR-2 molecule; demyelinating; multiple sclerosis; immune response; antiinflammatory; neuroprotective; proliferation; MHC class II protein inhibitor; demyelinating disease; inhibition; post-viral encephalomyelitis; post-vaccine demyelinating condition; anti-tumour necrosis factor agent.
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Pred. No. 0.0013;
2; Mismatches 0; Indels
                                                                                     HLA-DR2 molecule binding peptide SEQ ID NO:88.
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Best Local Similarity 86.7
Matches 13; Conservative
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                                                                                                                                                                                                                                                                       Synthetic.
                  ABP52294;
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Gaps ő

ABP52294 standard; peptide; 17 AA.

RESULT 5 ABP52294 ID ABP5:

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The present invention describes compositions (I) comprising a peptide with an amino acid sequence with tyrosine (Y), lysine (K), and/or valine residues. The complex of the peptide with a major histocompatibility complex (MHC) class II HLA-DR2 protein is involved in modulating an immune response. (I) has antiinflammatory and neuroprotective activities, and can be used as MHC class II protein inhibitor. The compositions comprising the peptides are useful for treating demyelinating diseases such as multiple sclerosis, post-viral encephalomyelitis, a post-vaccine demyelinating condition, and a side effect of administering an antituour necrosis factor agents. The peptide further inhibits prollication of autoantigen-specific HLA-DR2.restricted T cell clones. ABP52207 to ABP52305 represent peptides used in the exemplification of the present
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Human leukocyte antigen; HLA; major histocompatibility complex; MHC; HLA-DR2; MHC class II DR-2 molecule; demyelinating; multiple sclerosis; immune response; antiinflammatory; neuroprotective; proliferation; MHC class II protein inhibitor; demyelinating disease; inhibition; post-viral encephalomyelitis; post-vaccine demyelinating condition;
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                                                                                                   anti-tumour necrosis factor agent
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86.7%;
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Best Local Similarity
Matches 13; Conserv
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The present invention describes compositions (I) comprising a peptide with an amino acid sequence with tyrosine (Y), lysine (K), and/or valine residues. The complex of the peptide with a major histocompatibility complex (MHC) class II MLA-DE2 protein is involved in modulating an immune response. (I) has antiinflammatory and neuroprotective activities, and can be used as AMC class II protein inhibitor. The compositions comprising the peptides are useful for treating demyelinating diseases such as multiple sclerosis, post-viral encephalomyelitis, a post-vaccine demyelinating condition, and a side effect of administering an anti-tumour necrosis factor agents. The peptide further inhibits proliferation of autoantigen-specific HIA-DEZ-restricted T cell clones. ABP52207 to
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Pred. No. 0.0014;
2; Mismatches 0; Indels
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                                                                                                                                                                                                         Fridkis-Hareli M;
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                                                                                                         24-JAN-2002; 2002WO-US002071.
                                                                                                                                         24-JAN-2001; 2001US-0263569P.
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Best Local Similarity 86.7
Matches 13; Conservative
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                                                                                                                                                                                                                                                                                                                       encephalomyelitis.
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Homo sapiens.
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The present invention describes compositions (I) comprising a peptide with an amino acid sequence with tyrosine (Y), lysine (K), and/or valine residues. The complex of the peptide with a major histocompatibility complex (MHC) class II HIA-DR2 protein is involved in modulating an immune response. (I) has antiinflammatory and neuroprotective activities, and can be used as MHC class II protein inhibitor. The compositions comprising the peptides are useful for treating demyelinating diseases such as multiple sclerosis, post-viral encephalomyelitis, a post-vaccine demyelinating condition, and a side effect of administering an anti-tumour necrosis factor agents. The peptide further inhibits proliferation of autoantigen-specific HIA-DR2-restricted T cell clones, ABB52207 to
                                                                                                           New compositions comprising synthetic peptides in complex with a major histocompatibility complex class II HLADR2 protein, useful for treating a demyelinating disease, e.g. multiple sclerosis, or post-viral encephalomyelitis.
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7; Mismatches
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                                                                                                                                                                                                                                                                                Claim 28; Page 39; 54pp; English.
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Best Local Similarity 80.09
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Pred. No. 0.0027;
1; Mismatches 1; Indels
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                                                                                                                                                                                                         Fridkis-Hareli M;
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24-JAN-2002; 2002WO-US002071
                                                                    24-JAN-2001; 2001US-0263569P
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EKAKFEAYKAAAAPA 17
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Matches 13; Conserv
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                                                                                                                                                                                                         Strominger JL,
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Query Match

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Gaps

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Length 15; 1; Indels

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New compositions comprising synthetic peptides in complex with a major histocompatibility complex class II HLADR2 protein, useful for treating a demyelinating disease, e.g. multiple sclerosis, or post-viral encephalomyelitis. Strominger JL, Fridkis-Hareli M; WPI; 2002-608439/65.

Fridkis-Hareli M;

Strominger JL,

24-JAN-2001; 2001US-0263569P

(HARD) HARVARD COLLEGE

24-JAN-2002; 2002WO-US002071

01-AUG-2002

Synthetic

Homo

ABP52270;

HLA-DR2

Sequence 15 AA;

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The present invention describes compositions (1) comprising a peptide with an amino acid sequence with tyrosine (Y), 19sine (X), and/or valine residues. The complex of the peptide with a major histocompatibility complex (MHC) class II HLA-DE2 protein is involved in modulating an immune response. (I) has antiinflammatory and neuroprotective activities, and can be used as a MHC class II protein inhibitor. The compositions comprising the peptides are useful for treating demyelinating diseases such as multiple sclerosis, post-viral encephalomyelitis, a post-vaccine demyelinating condition, and a side effect of administering an antitumour necrosis factor agents. The peptide further inhibits proliferation of autoantigen specific HLA-DE2-restricted T cell clones. ABP52207 to ABP52305 represent peptides used in the exemplification of the present
Claim 28; Page 39; 54pp; English
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81.2%; Score 56; DB 5; Length 15; 80.0%; Pred. No. 0.016; 2; Indels :ive 1; Mismatches 2; Indels || ||||:|||| | EKPKFEAYKAAAAPA 15 1 EKAKFEAFKAAAAA 15 Local Similarity 80.0 hes 12; Conservative Query Match Matches ઠ 셤

ABP52291 standard; peptide; 15 AA. (first entry) 16-OCT-2002 ABP52291; ABP5229

HLA-DR2 molecule binding peptide SEQ ID NO:85.

Human leukocyte antigen; HLA; major histocompatibility complex; MHC; HLA-DR2; MHC class II DR-2 molecule; demyelinating; multiple sclerosis; immune response; antinflammatory; neuroprotective; proliferation; MHC class II protein inhibitor; demyelinating disease; inhibition; post-varal encephalomyelitis; post-vaccine demyelinating condition; anti-tumour necrosis factor agent.

sapiens. Synthetic. Ношо

WO200259143-A2.

01-AUG-2002

24-JAN-2002; 2002WO-US002071.

24-JAN-2001; 2001US-0263569P.

(HARD) HARVARD COLLEGE

Strominger JL, Fridkis-Hareli M;

WPI; 2002-608439/65.

๙ New compositions comprising synthetic peptides in complex with a major. histocompatibility complex class II HLADR2 protein, useful for treating demyelinating disease, e.g. multiple sclerosis, or post-viral encephalomyelitis.

Claim 28; Page 39; 54pp; English.

The present invention describes compositions (I) comprising a peptide with an amino acid sequence with tyrosine (Y), lysine (K), and/or valine residues. The complex of the peptide with a major histocompatibility complex (MHC) class II HLA-DR2 protein is involved in modulating an

immune response. (I) has antiinflammatory and neuroprotective activities, and can be used as a MHC class II protein inhibitor. The compositions comprising the peptides are useful for treating demyelinating diseases such as multiple sclerosis, post-viral encephalomyelitis, a post-vaccine demyelinating condition, and a side effect of administering an antitumour necrosis factor agents. The peptide further inhibits proliferation of autoantigen-specific HLA-DR2-restricted T cell clones. ABP52207 to ABP52305 represent peptides used in the exemplification of the present invention 88888888888

Sequence 15 AA;

Gaps . 76.8%; Score 53; DB 5; Length 15; 73.3%; Pred. No. 0.049; 2; Indels cive 2; Mismatches 2; Indels 11; Conservative Query Match Best Local Similarity Matches

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1 EKAKFEAFKAAAAA 15 ò 셤

ABP52263 standard; peptide; 15 AA. RESULT 12 **ABP52263**

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Gaps ;

(first entry) 16-OCT-2002

Human leukocyte antigen; HLA; major histocompatibility complex; MHC; HLA-DR2; MHC class II DR-2 molecule; demyelinating; multiple sclerosis; immune response; antiinflammatory; neuroprotective; proliferation; MHC class II protein inhibitor; demyelinating disease; inhibition; post-viral encephalomyelitis; post-vaccine demyelinating condition; anti-tumour necrosis factor agent. HLA-DR2 molecule binding peptide SEQ ID NO:57.

Synthetic

WO200259143-A2.

01-AUG-2002

24-JAN-2002; 2002WO-US002071.

24-JAN-2001; 2001US-0263569P.

(HARD) HARVARD COLLEGE

Ξ Fridkis-Hareli Strominger JL,

WPI; 2002-608439/65.

New compositions comprising synthetic peptides in complex with a major histocompatibility complex class II HLADR2 protein, useful for treating a demyelinating disease, e.g. multiple sclerosis, or post-viral encephalomyelitis.

Example 1; Page 33; 54pp; English.

with an amino acid sequence compositions (1) lygine (K), and/or valine residues. The complex of the peptide with a major histocompatibility complex (MHC) class II HLA-DR2 protein is involved in modulating an immune response. (I) has antiinflammatory and neuroprotective activities, and can be used as a MHC class II protein inhibitor. The compositions comprising the peptides are useful for treating demyelinating diseases such as multiple scierosis, post-viral encephalomyelities, a post-vaccine demyelinating condition, and a side effect of administering an anti-tumour necrosis factor agents. The peptide further inhibits proliferation of autoantigen-specific HLA-DR2-restricted T cell clones. ABB52207 to The present invention describes compositions (I) comprising a

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ABP52305 represent peptides used in the exemplification of the present
                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                             Human leukocyte antigen; HLA; major histocompatibility complex; MHC;
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                                                                               Score 53; DB 5; Length 15;
Pred. No. 0.049;
3; Mismatches 1; Indels
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Pred. No. 0.072;
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                                                                                                 73.3%;
                                                                                 76.8%;
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75.4%;

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                                                                                                                                                                                                                                                      Human leukocyte antigen; HLA; major histocompatibility complex; MHC; HLA-DR2; MHC class II DR-2 molecule; demyelinating; multiple sclerosis; immune response; antinflammatory; neuroprotective; proliferation; MHC class II protein inhibitor; demyelinating disease; inhibition; post-viral encephalomyelitis; post-vaccine demyelinating condition;
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                                                                                                                   ABP52259 standard; peptide; 15 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Example 1; Page 33; 54pp; English.
                                                                                                                                                                                                                                                                                                                                                anti-tumour necrosis factor agent
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The present invention describes compositions (I) comprising a peptide with an amino acid sequence with tyrosine (Y), lysine (K), and/or valine residues. The complex of the peptide with a major histocompatibility complex (MHC) class II HLA-DE2 protein is involved in modulating an immune response. (I) has antiinflammatory and neuroprotective activities, and can be used as a MHC class II protein inhibitor. The compositions comprising the peptides are useful for treating demyelinating doils are useful for treating demyelinating doils are useful for treating demyelinating condition, and a side effect of administering an antitumour necrosis factor agents. The peptide further inhibits proliferation of autoantigen-specific HLA-DR2-restricted T cell clones. ABB52207 to
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                                                                                                                                                                                                                                                                                                      HLA-DR2 molecule binding peptide SEQ ID NO:51.
                                                                           ABP52257 standard; peptide; 15 AA
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RESULT 15
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Query Match 73.9%; Score 51; DB 5; Length 15;
Best Local Similarity 73.3%; Pred. No. 0.11;
Matches 11; Conservative 2; Mismatches 2; Indels 0; Gaps
Qy 1 EKAKFEAFKAAAAA 15

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Db 1 BAAKYAAYKAAAAA 15

Search completed: March 31, 2005, 02:35:28 Job time : 88.7903 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on:

March 31, 2005, 02:26:53 ; Search time 22.9839 Seconds (without alignments) 48.718 Million cell updates/sec

US-10-056-583A-95 69 1 EKAKFEAFKAAAAA 15 Title: Perfect score:

Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

513545 seqs, 74649064 residues Searched:

513545 Total number of hits satisfying chosen parameters:

length: 0 length: 2000000000 Minimum DB seq Maximum DB seq

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

Issued Patents AA:*

(Ggn2_6/ptodata/1/iaa/5A_COMB.pep:*
(Ggn2_6/ptodata/1/iaa/5B_COMB.pep:*
(Ggn2_6/ptodata/1/iaa/6A_COMB.pep:*
(Ggn2_6/ptodata/1/iaa/6B_COMB.pep:*
(Ggn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
(Ggn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

STIMMARTES

SUMMARIES	n DB ID Description	4 US-09-248-796A-18658 Sequence	4 US-09-252-991A-22139 Sequence 22139,	4 US-09-489-039A-13950 Sequence 1395	5 PCT-US95-04121-38	1 US-08-295-670-6 Sequence 6, 7	1 US-08-633-485-6 Sequence 6,	3 US-08-508-761B-4 Sequence 4,	3 US-09-117-121-16 Seguence 16,	3 US-09-117-121-24 Sequence 24	4 US-09-344-529-5 Sequence 5, 1	4 US-09-248-796A-25516 Sequence	4 US-09-198-452A-1021 Sequence	4 US-09-438-185A-950 Sequence 950, 7	4 US-09-543-681A-7747 Sequence 7747	4 US-09-328-352-4241	5 PCT-US94-10257A-33 Sequence 33,	3 US-09-117-121-30 Sequence 30,	4 US-09-732-210-1445 Sequence 1445	6 5273901-7 Patent No. 5273	6 5482709-6 Patent No.	0 6 5273901-7 Patent No. 5273901	6 5482709-6 Patent No.	4 US-09-328-352-4239 Seguence 4239	4 US-09-919-497-100 Sequence 100, P	4 US-09-060-450-5 Sequence 5, A	4 TIS-00-40E-742A-7	'/ acreman /-wet/-cot-co t
	Query Match Length	1001	166	466	13	497	497	510	38	38	38	69	476	479	576	759	13	24	162	180	180	180	180	405	582	10	109	
de	Query Match	58.0	56.5	56.5	55.1	55.1	55.1	55.1	53.6	53.6	53.6	53.6	53.6	53.6	53.6	53.6	52.2	52.2	52.2	52.2	52.2	52.2	52.2	52.2	52.2	50.7	50.7	
	Score	40	39	39	38	38	38	38	37	37	37							36						36				
	Result No.	п	7	Э	4	.co	9	7	80	6	10	11	12	13	14	15	16	17	18	19	, 20	21	22	23	24	25	56	

equence 5527, Ap	equence 11599, A	equence 16623, A	equence 3759, Ap	Sequence 4, Appli	Sequence 7, Appli	Sequence 7, Appli	Sequence 7, Appli	Sequence 26859, A	~	Sequence 7165, Ap	sequence 6873, Ap	equence 8171, Ap	equence 26, Appl	Sequence 171, App	Sequence 152, App	Sequence 40, Appl	Sequence 1, Appli
Seq	Sed	Sed	Sed	Sed	Sed	Seg	Sed	Sed	Sed	Sed	Sed	Sed	Sed	Sed	Sed	Sed	Seq
US-09-513-999C-5527	US-09-902-540-11599	US-09-902-540-16623	US-09-134-000C-3759	US-07-637-870-4	US-07-637-399-7	US-07-640-476-7	US-08-112-703-7	US-09-252-991A-26859	US-09-134-078-20	US-09-949-016-7165	US-09-543-681A-6873	US-09-489-039A-8171	US-09-673-198-26	US-09-198-452A-171	US-09-438-185A-152	US-09-345-473E-40	US-09-411-578-1
4	4	4	4	Н	7	Н	Т	4	٣	4	4	4	4	4	4	4	m
143	171	219	249	388	388	388	388	409	454	457	474	607	637	1156	1562	1601	214
50.7	50.7	50.7	50.7	50.7	50.7	50.7	50.7	50.7	50.7	50.7	50.7	50.7	50.7	50.7	50.7	50.7	50.0
35	35	35	35	35	35	35	35	35	35	35	35	35	35	35	35	35	34.5
28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

US-09-248-796A-18658

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Sequence 18658, Application US/09248796A

Patent No. 6747137
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: NUCLEIC ACID AND THERAPEUTICS
TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: WHERE: US/09/248,796A
CURRENT FILING DATE: 1999-02-12
PRIOR PAPLICATION NUMBER: US 60/074,725
PRIOR PAPLICATION NUMBER: US 60/074,725
PRIOR FILING DATE: 1998-02-13
NUMBER OF SEQ ID NOS: 28208
SEQ ID NO 18658
LENGTH: 1001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; OTHER INFORMATION: Identity of amino acid sequences at the above locations are unkno
US-09-248-796A-18658
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 22139, Application US/09252991A
Sequence 22139, Application US/09252991A
Fatent No. 6551795
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS;
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: ABUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
FRIOR RAPLICATION NUMBER: US 60/074,788
FRIOR FILING DATE: 1998-02-18
FRIOR FILING DATE: 1998-07-27
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 40; DB 4; Length 1001;
Pred. No. 1.6e+02;
0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   58.0%;
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818 KAKEEAEAAAAAA 831
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2 KAKFEAFKAAAAA 15
                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: PRT
ORGANISM: Candida albicans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       11, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity
Matches 11, Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME/KEY: UNSURE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 2
US-09-252-991A-22139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LOCATION:
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Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 497;
                                                                                                                                                                                       Score 38; DB 5; Length 13;
Pred. No. 4.6;
2; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STREET: 1755 S. Jefferson Davis Highway, Suite 400 STRET: Arlington STATE: Virginia COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ZIP: 22202
COMPUTER READABLE FORM:
MEDLUM TYPE: Floppy disk
COMPUTER: Ploppy disk
COMPUTER: Ploppy disk
COMPUTER: Parent Poc-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/295,670
FILING DATE: 08-SEP-1994
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
APPLICANT: KAMASAKI, HISASHI
APPLICANT: TSUCHIYA, MAKOTO
APPLICANT: MIWA, KIYOSHI
APPLICANT: KAWAHARA, YOSHIO
TITLE OF INVENTION: THE NOVEL CELL SURFACE PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   55.1%; Score 38; DB 1; 53.3%; Pred. No. 1.6e+02; tive 3; Mismatches 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRICATION 1973
PRICATION 1973
PRICATION NUMBER: PCT/JP94/00039
FILING DATE: 13-JAN-1994
PRICATION NUMBER: 13-JAN-1994
APPLICATION NUMBER: JP 5-4069
FILING DATE: 13-JAN-1993
ATTORNEY/AGENT INFORMATION:
NAME: Oblon, No. 5547864man F.
REGISTATION NUMBER: 24,618
REFERENCE/DOCKET NUMBER: 10-697-0 PCT
TELECOMMUNICATION, INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    10-697-0 PCT
                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 6, Application US/08295670
Patent No. 5547864
                                                                                                                                                                                              55.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEPHONE: (703) 413-3000
TELEFAX: (703) 413-220
TELEX: 248855 OPAT UR
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 EKAKFEAFKAAAAA 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               : 497 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 53.3%
            13 amino acids
                                                                                                                                                                                         Query Match
Best Local Similarity 69.2
Matches 9; Conservative
                                                                                                                                                                                                                                                                                       3 AKFEAFKAAAAA 15
                                                                                                                                                                                                                                                                                                                  | ::| |||||||
1 AAYKAAKAAAAA 13
                                                                                              MOLECULE TYPE: peptide
; FRAGMENT TYPE: internal
PCT-US95-04121-38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             / MOLECULE TYPE: protein US-08-295-670-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
ADDRESSEE: OBLON, SP
ADDRESSEE: P.C.
                                 TYPE: amino acid
STRANDEDNESS:
                                                                               linear
                                                                             TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                            JS-08-295-670-6
            LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 5
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Sequence 13950, Application US/09489039A

Patent No. 6610836

Batent No. 6610836

Batent No. 6610836

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA CURRENT APPLICATION NUMBER: US 60489,039A

CURRENT FILING DATE: 1099-01-29

RIOR FILING DATE: 1999-01-29

NUMBER OF SEQ ID NOS: 14342

SEQ ID NO 13950
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NUMBER OF SEQUENCES: 62
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN PC-DOS/MS-DOS
SOFTWARE: PATENTIN PC-DOS/MS-DOS
CURRENT APPLICATION NUMBER: PCT/US95/04121
FILING DATE:
RIGHT APPLICATION:
PRIOR APPLICATION NUMBER: 08/222,206
FILING DATE: 08/222,206
FILING DATE: MAPPLICATION NUMBER: 08/222,206
                                                                                                                                                                 Score 39; DB 4; Length 166;
Pred. No. 39;
2; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 39; DB 4; Length 466; Pred. No. 1.1e+02; 0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Vanstone, Darlene A.
REGISTRATION NUMBER: 35,279
REFERENCE/DOCKET NUMBER: 079.2PCT
TELECOMMUNICATION INPORMATION:
TELEPHONE: (617) 466-6010
TELEPHONE: (617) 466-6010
INPORMATION FOR SEQ ID NO: 38:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 38, Application PC/TUS9504121 GENERAL INFORMATION: APPLICANT:
                                                                        ; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-22139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: PRT
ORGANISM: Klebsiella pneumoniae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          56.5%;
76.9%;
                                                                                                                                                               Query Match
Best Local Similarity 64.3%;
Matches 9; Conservative
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104 KAQVDAFHAAALAA 117
                                                                                                                                                                                                                                                          2 KAKFEAFKAAAAA 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 153 ASLEAQKAAAAA 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3 AKFEAFKAAAAA 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          10; Conservative
NUMBER OF SEQ ID NOS:
SEQ ID NO 22139
LENGTH: 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity
Matches 10, Conserv
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PCT-US95-04121-38
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                                                                                                     GENERAL INFORMATION:
APPLICANT: KAWASAKI, HISASHI
APPLICANT: TSUCHIYA, NAKOTO
APPLICANT: MWA, KIYOSHI
APPLICANT: KAWAHARA, YOSHIO
TITLE OF INVENTION: THE NOVEL CELL SURFACE PROTEIN
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
ADDRESSE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE: USECTORY, CALLER ADDRESSEE: USECTORY: ALTHOROM STREET: 1755 S. Jefferson Davis Highway, Suite 400 CITY: Artington STATE: Urginia COUNTRY: U.S.A.

ZTATE: Virginia COUNTRY: U.S.A.

ZTATE: Virginia COUNTRY: U.S.A.

COMPUTER READABLE FORM:
MEDIUM TYPE: Ploppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PETENTON DATA:
APPLICATION NUMBER: US/08/633,485
FILING DATE: 17-APR-1996
FILING DATE: 13-APR-1994
APPLICATION NUMBER: US 08/295,670
FILING DATE: 13-JAN-1994
APPLICATION NUMBER: US 08-296
FILING DATE: 13-JAN-1994
APPLICATION NUMBER: US 6807-0 PCT
FILING DATE: 13-JAN-1993
ATTORNEY/AGENT INFORMATION:
MESTIVE APPLICATION NUMBER: 10-697-0 PCT
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    55.1%; Score 38; DB 1; Length 497; 53.3%; Pred. No. 1.6e+02; tive 3; Mismatches 4; Indels
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Patent No. 6027920
GENERAL INFORMATION:
APPLICANT: Joliff, Gwennael
APPLICANT: Guyonvarch, Armel
APPLICANT: Purification, Relano
APPLICANT: Duchiron, Francis
US-08-633-485-6
; Sequence 6, Application US/08633485
; Patent No. 5681717
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amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 53.37
Best Local 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            , MOLECULE TYPE: protein
US-08-633-485-6
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Sequence 16, Application US/09117121

Patent No. 6307020

GENERAL INFORMATION:

APPLICANT: How, Choy

APPLICANT: Gong, Zhiyuan

TITLE OF INVENTION: Intracellular Antifreeze Polypeptides

TITLE OF INVENTION: and Nucleic Acids

NUMBER OF SEQUENCES: 46

CORRESPONDENCE ADDRESS:

ADDRESSEE: Townsend and Townsend and Crew LLP

STREET: Two Embarcadero Center, Eighth Floor

CITY: San Francisco

STATE:..California

COUNTRY: 'USA.
System for Protein Expression and
Secretion Especially in Corynebacteria
37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 510;
                                                                                                                         ADDRESSEE Jacobson, Price, Holman & Stern, PLLC STREET: 400 Seventh St. N.W.

CITY: Washington D.C.

COUNTRY: U.S.A.

ZIP: 20004

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER READABLE FORM:

MEDIUM TYPE: Ploppy disk

COMPUTER: BAFFICATION DATA:

APPLICATION NUMBER: US/08/508,761B

FILING DATE: 31-JUL-1995

PRICH APPLICATION DATA:

APPLICATION NUMBER: FR 91/09652

FILING DATE: 29-JUL-1991

PRICH APPLICATION NUMBER: FR 91/09670

FILING DATE: 29-JUL-1991

PRICH APPLICATION NUMBER: FR 91/09670

FILING DATE: 31-409

REGISTRATION NUMBER: FR 91/09670

FILING DATE: 02-MG-1991

ATCORNEY, AGENT INFORMATION:

NAME: Player, William E

REGISTRATION NUMBER: 31,409

REGISTRATION NUMBER: 91,09870

FILING DATE: 02-MG-1991

ATCORNEY, AGENT INFORMATION:

NAME: Player, William E

REGISTRATION NUMBER: 91,409

REFERENCE/DOCKET NUMBER: PS8525NA

TELECOMMUNICATION INFORMATION:

TELEPHONE: (202) 638-6666
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OPERATING SYSTEM: PC_DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/117,121
FILING DATE: 20-NOV-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 55.1%; Score 38; DB 3; I Best Local Similarity 53.3%; Pred. No. 1.7e+02; Matches 8; Conservative 3; Mismatches 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
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104 EQAAYEAFEAARVRA 118
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TELEFAX: (202) 393-5350
INFORMATION FOR SEQ ID NO: 4
Renaud, Michel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         510 amino acids
                    TITLE OF INVENTION: SYST.
TITLE OF INVENTION: Secr.
NUMBER OF SEQUENCES: 37
CORRESPONDENCE ADDRESS:
ADDRESSEE: Jacobson, P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS:
LENGTH: 510 amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY:
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Gaps

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Indels

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Pred. No. 19; 0; Mismatches

71.4%;

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10; Conservative
               Best Local Similarity
Matches 10; Conserv
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| Patent No. 6307020
| GENERAL INPORMATION:
| APPLICANT: Hew, Choy
| TITLE OF INVENTION: Intracellular Antifreeze Polypeptides
| TITLE OF INVENTION: and Nucleic Acids
| VINER OF SEQUENCES: 46
| NUMBER OF SEQUENCES: 46
| CORRESPONDENCE ADDRESS:
| ADDRESSEE: Townsend and Townsend and Crew LLP
| STREET: Two Embarcadero Center, Eighth Floor
| CITY: San Francisco
| STARET: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 37; DB 3; Length 38;
Pred. No. 19; 4; Indels
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PRIOR APPLICATION DATA:
APPLICATION DAMA:
ATTORIEN TO NUMBER: WO PCT/CA97/00062
FILING DATE: 30-JAN-1997
ATTORIEY/AGENT INFORMATION:
NAME: Weber, Kenneth A.
REGISTRATION NUMBER: 31,677
REFRENCE/DOCKET NUMBER: 016252-001610US
TELEPHONE: (415) 576-0300
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
CLEMCATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
CHARACT
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REGISTRATION NUMBER: 31,677
REFERENCE/DOCKET NUMBER: 016252-001610US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 53.6%;
Best Local Similarity 71.4%;
Matches 10; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MOLECULE TYPE: protein US-09-117-121-16
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US-09-117-121-24
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53.6%; Score 37; DB 3; Length 38;

Query Match

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Sequence 25516, Application US/09248796A

Batent No. 6747137
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
CURRENT APPLICATION NUMBER: US/09/248,796A
CURRENT FILING DATE: 1999-02-12
CURRENT FILING DATE: 1998-02-13
PRIOR PAPLICATION NUMBER: US 60/074,725
PRIOR PAPLICATION NUMBER: US 60/074,725
PRIOR FILING DATE: 1998-02-13
PRIOR FILING DATE: 1998-02-13
NUMBER OF SEQ ID NOS: 28208
SEQ ID NO 25516
LENGTH: 69
                                                                                                                                        US-09-344-529-5
; Sequence 5, Application US/09344529
; Sequence 5, Application US/09344529
; Patent No. 64252933
; GENERAL INFORMATION:
; APPLICANT: Hew, Choy L.
; APPLICANT: Hew, Choy L.
; APPLICANT: Hew, Choy L.
; APPLICANT: HEW Research and Development Limited Partnership
; TILLE OF INVENTION: Sculpin-Type Artifreeze Polypeptides and Nucleic Acids
; TILE REFERENCE: 0.16252-002620US
; CURRENT APPLICATION NUMBER: US/09/344,529
; CURRENT PILING DATE: 1999-06-26
; EARLIER PILING DATE: 1998-06-26
; RARLIER PILING DATE: 1998-08-07
; NUMBER OF SEQ ID NOS: 19
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OTHER INFORMATION: Winter flounder skin-type antifreeze polypeptide
OTHER INFORMATION: (wfgAFP-1)
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Best Local Similarity 71.4%;
Matches 10; Conservative
2 KAKFEAFKAAAAA 15
                                                 16 KAAAEATKAAAKA 29
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8 EAKLDTFPAAATAA 21
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SEQ ID NO 5
LENGTH: 38
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ORGANISM: Candida albicans
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Best Local Similarity 57.1
Matches 8; Conservative
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US-09-248-796A-25516
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TITLE OF INVENTION:
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US-09-328-352-4241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: PRT
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                                                                                         Sequence 1021, Application US/09198452A
Patent No. 6559294
BARRATION: GENERAL INFORMATION:
APPLICANT: Griffals,
APPLICANT: Griffals,
TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragments
TITLE OF INVENTION: thereof and uses thereof, in particular for the diagnosis, prevering RILE REPERENCE: 9710-003-999
CURRENT APPLICATION NUMBER: US/09/198,452A
CURRENT FILING DATE: 1998-11-24
NUMBER OF SEQ ID NOS: 6849
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; Sequence 7747, Application US/09543681A
; Sequence 7787, Application US/09543681A
; Sequence 7787, Seque
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APPLICANT: Stephens, Richard
APPLICANT: Mitchell, Wayne
APPLICANT: Mitchell, Wayne
APPLICANT: Mitchell, Wayne
APPLICANT: Malman, Sue
APPLICANT: Davis, Ronald
APPLICANT: Davis, Ronald
TITLE OF INVENTION: Chlamydia Pneumoniae Genome Sequence
FILE REFERENCE: 018941-000411US
CURRENT APPLICATION NUMBER: US/09/438,185A
CURRENT APPLICATION NUMBER: US 60/108,279
PRIOR PPLING DATE: 1998-11-12
PRIOR PPLING DATE: 1999-11-12
PRIOR PLING DATE: 1999-04-08
NUMBER OF SEQ ID NOS: 1074
SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      53.6%; Score 37; DB 4; Length 479; 72.7%; Pred. No. 2.3e+02; ive 1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         53.6%; Score 37; DB 4; Length 476; 72.7%; Pred. No. 2.3e+02;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; Sequence 950, Application US/09438185A; Patent No. 6822071
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: PRT ORGANISM: Chlamydia pneumoniae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: PRT
ORGANISM: Chlamydia pneumoniae
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US-09-438-185A-950
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity 72.7
Matches 8; Conservative
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Matches 8; Conservative
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110 RFSAFAAAAA 120
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                               RESULT 12
US-09-198-452A-1021
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-09-198-452A-1021
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 13
US-09-438-185A-950
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Sequence 421, Application US/09328352

Retent No. 6562958

GENERAL INFORMATION:

APPLICANT: GATY L. Breton et al.

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER

TITLE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS

TITLE OF INVENTION: DADARS: US/09/328,352

CURRENT APPLICATION NUMBER: US/09/328,352

CURRENT FILING DATE: 1999-06-04

SEQ ID NO 4241

LENGTH: 759
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                                                                                                                                                                                                                                                                          Length 576;
                                                                                                                                                                                                                                                    Score 37; DB 4; Length 5.c. Pred. No. 2.7e+02;
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DIAGNOSTICS AND THERAPEUTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 37; DB 4; I
Pred. No. 3.6e+02;
0; Mismatches 4;
                                                                                                                                                                                                                                                                                                                  4; Mismatches
             FILE REFERENCE: 2709.1002-001
CURRENT APPLICATION NUMBER: US/09/543,681A
CURRENT FILING DATE: 2000-04-05
PRIOR APPLICATION NUMBER: US 60/128,706
PRIOR FILING DATE: 1999-04-09
NUMBER OF SEQ ID NOS: 8344
LENGTH: 576
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Search completed: March 31, 2005, 02:44:10 Job time : 23.9839 secs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        , ORGANISM: Acinetobacter baumannii
US-09-328-352-4241
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Best Local Similarity 71.4%;
Matches 10; Conservative
                                                                                                                                                                                                                                                                        Query Match 53.6%;
Best Local Similarity 50.0%;
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                    311 EEEOFOAYKAVAEA 324
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                                                                                                                                                                                       ; TYPE: PRT
; ORGANISM: Proteus mirabilis
US-09-543-681A-7747
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March 31, 2005, 02:29:23 ; Search time 66.5323 Seconds (without alignments) 74.648 Million cell updates/sec
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1: /cgn2_6/ptodata/2/pubpaa/VESO7 PUBCOMB.pep:*
2: /cgn2_6/ptodata/2/pubpaa/PCT NEW PUB.pep:*
4: /cgn2_6/ptodata/2/pubpaa/NESO6 NEW PUB.pep:*
5: /cgn2_6/ptodata/2/pubpaa/NESO7 NEW PUB.pep:*
5: /cgn2_6/ptodata/2/pubpaa/NESO7 NEW PUB.pep:*
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7: /cgn2_6/ptodata/2/pubpaa/NESOR PUBCOMB.pep:*
8: /cgn2_6/ptodata/2/pubpaa/NESOR PUBCOMB.pep:*
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10: /cgn2_6/ptodata/2/pubpaa/NESOR PUBCOMB.pep:*
11: /cgn2_6/ptodata/2/pubpaa/NESOR PUBCOMB.pep:*
12: /cgn2_6/ptodata/2/pubpaa/NESOR PUBCOMB.pep:*
13: /cgn2_6/ptodata/2/pubpaa/NESOR PUBCOMB.pep:*
14: /cgn2_6/ptodata/2/pubpaa/NESOR PUBCOMB.pep:*
15: /cgn2_6/ptodata/2/pubpaa/NESOR PUBCOMB.pep:*
16: /cgn2_6/ptodata/2/pubpaa/USIOP_PUBCOMB.pep:*
17: /cgn2_6/ptodata/2/pubpaa/USIOP_PUBCOMB.pep:*
18: /cgn2_6/ptodata/2/pubpaa/USIOP_PUBCOMB.pep:*
18: /cgn2_6/ptodata/2/pubpaa/USIOP_PUBCOMB.pep:*
19: /cgn2_6/ptodata/2/pubpaa/USIOP_PUBCOMB.pep:*
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      .1407402 seqs, 331100923 residues
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                                      OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 2000000000
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Sequence:
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                                                                                                                                                                                                                  Run on:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

		Appl												
	_	95,	96	65,	88	90,	89,	97,	64,	92,	91,	57,	85,	, 99
	Description	Seguence	Sequence											
	ΩI	US-10-056-583-95	US-10-056-583-96	US-10-056-583-65	US-10-056-583-88	US-10-056-583-90	US-10-056-583-89	US-10-056-583-97	US-10-056-583-64	US-10-056-583-92	US-10-056-583-91	US-10-056-583-57	US-10-056-583-85	US-10-056-583-66
	DB	14	14	14	14	14	14	14	14	14	14	14	14	14
	Query Match Length DB	15	17	15	17	17	19	17	15	15	15	15	15	15
*	Query	100.0	92.8	91.3	91.3	91.3	91.3	88.4	82.6	82.6	81.2	76.8	76.8	75.4
	Score	69	64	63	63	63	63	61	57	57	26	53	53	25
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51, 53, 94, 98,	equence 93, equence 33, equence 45, equence 47,	9,00°,00°,00°,00°,00°,00°,00°,00°,00°,00	30,0	Sequence 59, Appl Sequence 71, Appl Sequence 74, Appl Sequence 34, Appl Sequence 35, Appl	4444	99, 1412 1412 24, A 24,
10-056-583- 10-056-583- 10-056-583-	10-056-583-9 10-056-583-3 10-056-583-4 10-056-583-4	056-5 -056-5 -056-5 -056-5		-056-5	10-056- 10-056- 10-056-	-10-056- -10-437- -10-437- 09-765-3
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ALIGNMENTS

RESULT. 1 US-10-056-583-95 Squence 95, Application US/10056583 Publication No. US20030064915A1 GENERAL INFORMATION: APPLICANT: Presidents and Fellows of Harvard College APPLICANT: Strominger, Jack L. APPLICANT: Strominger, Jack L. TITLE OF INVENTION: THERAPEUTIC PEPTIDES FOR DEMYELINATING TITLE OF INVENTION: CONDITIONS FILE REFERRENCE: 24655-017 TITLE OF INVENTION: CONDITIONS FILE OF INVENTION: CONDITIONS FILE OF INVENTION: CONDITIONS FILE OF INVENTION: CONDITIONS FILE OF INVENTION: HOWBER: 06/263,569 FRIOR APPLICATION NUMBER: 60/263,569 FRIOR PILING DATE: 2001-01-24 PRIOR FILING DATE: 2001-01-24 NUMBER OF SEQ ID NOS: 99 SOFTWARE: FastSEQ for Windows Version 4.0 SEQ ID NOS: 99 SOFTWARE: PRT ORGANISM: Artificial Sequence FEATURE: OTHER INFORMATION: The peptide was designed and synthesized. US-10-056-583-95 QUERY MATCH Best Local Similarity 100.0%; Pred. No. 5.5e-05; Matches 15; Conservative 0; Mismatches 0; Indels ON I EKAKFEAFKAAAAAA 15 DD REVAREMENTALE OF SEQ 100 Mismatches 0; Indels NO I EKAKFEAFKAAAAAA 15

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RESULT 2 US-10-056-583-96

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US-10-056-583-90

i Sequence 90, Application US/10056583

j Sequence 90, Application US/10056583

j Publication No. US20030064915A1

j GENERAL INFORMATION:

j APPLICANT: Priodkis-Tareali Masha

TITLE OF INVENTION: THERAPEUTIC PEPTIDES FOR DEMYELINATING

TITLE OF INVENTION: CONDITIONS

FILE REPERENCE: 24655-017

CURRENT APPLICATION NUMBER: US/10/056,583

CURRENT FILING DATE: 2002-01-24

PRIOR FILING DATE: 2001-01-24

PRIOR FILING DATE: 2001-01-24

NUMBER OF SEQ ID NOS: 99

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 90

LENGTH: 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FEATURE: OTHER INFORMATION: The peptide was designed and synthesized.
                                                                                                                                                                                                                                                                                                                                                                               ; OTHER INFORMATION: The peptide was designed and synthesized US-10-056-583-88
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     91.3%; Score 63; DB 14; Length 17; 86.7%; Pred. No. 0.00063;
          APPLICANT: Fridkis-Hareli, Masha
TITLE OF INVENTION: THERAPEUTIC PEPTIDES FOR DEMYELINATING
TITLE OF INVENTION: CONDITIONS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Presidents and Fellows of Harvard College APPLICANT: Strominger, Jack L. APPLICANT: Strominger, Jack L. APPLICANT: Strominger, Jack L. APPLICANT: Fiddis-Hareli, Masha TITLE OF INVENTION: THERAPEUTIC PEPTIDES FOR DEMYELINATING FILE REPERRACE. 24655-017 CURRENT APPLICATION NUMBER: US/10/056,583
                                                                                                                                                                                                                                                                                                                                                                                                                                     91.3%; Score 63; DB 14; Ld
86.7%; Pred. No. 0.00063;
Mismarches 0;
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                                                                          CURRENT APPLICATION NUMBER: US/10/056,583
CURRENT FILMS DATE: 2002-01-24
PRIOR APPLICATION NUMBER: 60/263,569
PRIOR PILING DATE: 2001-01-24
NUMBER OF SEQ ID NOS: 99
SOFTWARE: FRRESEQ for Windows Version 4.0
LENGTH: 17
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Publication No. US20030064915A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                              ORGANISM: Artificial Sequence FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: PRT
ORGANISM: Artificial Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 91.3
Best Local Similarity 86.7
Matches 13; Conservative
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Matches 13; Conservative
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0
                                                                                            APPLICANT: Strominger, Jack L.
APPLICANT: Fridkis-Hareli, Masha
TITLE OF INVENTION: THERREPUIC PEPTIDES FOR DEMYELINATING
TITLE OF INVENTION: CONDITIONS
FILE REFERENCE: 24655-017
CURRENT APPLICATION NUMBER: US/10/056,583
CURRENT PILING DATE: 2002-01-24
PRIOR APPLICATION NUMBER: 60/263,569
PRIOR APPLICATION NUMBER: 60/263,569
PRIOR APPLICATION NUMBER: 60/263,569
NUMBER OF SEQ ID NOS: 99
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 96
LENGTH: 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Presidents and Fellows of Harvard College
APPLICANT: Strominger, Jack L.
APPLICANT: Strominger, Jack L.
APPLICANT: Fridkis-Hareli, Masha
TITLE OF INVENTION: THERAPEUTIC PEPTIDES FOR DEMYELINATING
TITLE OF INVENTION: CONDITIONS
FILE REPREMENT: 24655-017
CURRENT APPLICATION NUMBER: US/10/056,583
CURRENT PILING DATE: 2002-01-24
PRIOR APPLICATION NUMBER: 60/263,569
PRIOR FILING DATE: 2001-01-24
NUMBER OF SEQ ID NOS: 99
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 65
LENGTH: 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OTHER INFORMATION: The peptide was designed and synthesized
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OTHER INFORMATION: The peptide was designed and synthesized
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          92.8%; Score 64; DB 14; Length 17, 93.3%; Pred. No. 0.00043; Live 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      91.3%; Score 63; DB 14; Length 15;
86.7%; Pred. No. 0.00055;
tive 2; Mismatches 0; Indels
Sequence 96, Application US/10056583
Publication No. US20030064915A1
GENERAL INFORMATION:
APPLICANT: Presidents and Fellows of Harvard College
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-10-056-583-65; Sequence 65, Application US/10056583; Publication No. US20030064915A1; GENERAL INFORMATION:
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Publication No. US20030064915A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: PRT
ORGANISM: Artificial Sequence
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Matches 13; Conserv
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US-10-056-583-88
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Gaps

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FEATURE:

Matches

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Gaps

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APPLICANT: Presidents and Fellows of Harvard College APPLICANT: Strominger, Jack L.

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TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
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      SEQ ID NO 64
LENGTH: 15
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Publication No. US20030064915A1

GENERAL INFORMATION:

APPLICANT: Presidents and Fellows of Harvard College
APPLICANT: Strominger, Jack L.

APPLICANT: Stridkis-Harabeli, Masha
TITLE OF INVENTION: CONDITIONS

FILE REFERENCE: 2465-017

CURRENT APPLICATION NUMBER: US/10/056,583

CURRENT FILING DATE: 2002-01-24

PRIOR FILING DATE: 2001-01-24

NUMBER OF SEQ ID NOS: 99

SOFTWARE: FastSEQ for Windows Version 4.0

LENGTH: 17
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; Sequence 64, Application US/10056583
; Publication vo. US20030064915A1
; Publication vo. US20030064915A1
; GENERAL INFORMATION:
; APPLICANT: Presidents and Fellows of Harvard College
; APPLICANT: Strominger, Jack L.
; APPLICANT: Fridkis-Hareli, Masha
; TITLE OF INVENTION: THERAPECTIC PEPTIDES FOR DEMYELINATING
; TITLE OF INVENTION: THERAPECTIC PEPTIDES FOR DEMYELINATING
; TITLE OF INVENTION: CONDITIONS
; FILE REFERENCE: 24655-017
; CURRENT APPLICATION NUMBER: US/10/056,583
; CURRENT PILING DATE: 2001-01-24
; PRIOR FILING DATE: 2001-01-24
; NUMBER OF SEQ ID NOS: 99
; SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                       , OTHER INFORMATION: The peptide was designed and synthesized.
US-10-056-583-89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; OTHER INFORMATION: The peptide was designed and synthesized US-10-056-583-97
                                                                                                                                                                                                                                                                     91.3%; Score 63; DB 14; Length 19;
86.7%; Pred. No. 0.00071;
tive 2; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 61; DB 14; Length 17;
Pred. No. 0.0014;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1; Mismatches
                                                       NUMBER OF SEQ ID NOS: 99
SOFTWARE: FastSEQ for Windows Version 4.0'
SEQ ID NO 89
LENGTH: 19
CURRENT FILING DATE: 2002-01-24
PRIOR APPLICATION NUMBER: 60/263,569
PRIOR FILING DATE: 2001-01-24
                                                                                                                                        TYPE: PRT
ORGANISM: Artificial Sequence
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Best Local Similarity 86.74
Matches 13, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 86.7
Matches 13; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 7
US-10-056-583-97
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                                                                                                                                                                                     FEATURE:
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                                                                                                                                                                                                                                                                                                                                                                                        Sequence 92, Application US/10056583

Publication No. US20030064915A1

GENERAL INFORMATION:

APPLICANT: Presidents and Fellows of Harvard College

APPLICANT: Fridkis-Hareli, Masha

TITLE OF INVENTION: CONDITIONS

FILE REFERENCE: 24655-017

CURRENT APPLICATION NUMBER: US/10/056,583

CURRENT APPLICATION NUMBER: US/10/056,583

CURRENT APPLICATION NUMBER: 60/263,569

PRIOR APPLICATION NUMBER: 60/263,569

PRIOR PILING DATE: 2001-01-24

NUMBER OF SEQ ID NOS: 99

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ 1D NO 92
                                              ; FEATURE:
; OTHER INFORMATION: The peptide was designed and synthesized.
US-10-056-583-64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OTHER INFORMATION: The peptide was designed and synthesized
                                                                                                                                            Score 57; DB 14; Length 15;
Pred. No. 0.0056;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     82.6%; Score 57; DB 14; Length 15;
86.7%; Pred. No. 0.0056;
tive 1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 91, Application US/10056583

Publication No. USZ0030064915A1

GENERAL INFORMATION:
APPLICANT: Presidents and Fellows of Harvard College
APPLICANT: Friedkies-Hareli, Masha
TITLE OF INVENTION: THERAPEUTIC PEPTIDES FOR DEMYELINATING
TITLE OF INVENTION: CONDITIONS
                                                                                                                                                                                             Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION NUMBER: US/10/056,583
CURRENT FILING DATE: 2002-01-24
FRIOR APPLICATION NUMBER: 60/263,569
FRIOR FILING DATE: 2001-01-24
NUMBER OF SEQ ID NOS: 99
SOFTWARE: PastSEQ for Windows Version 4.0
SEQ ID NO 91
LENGTH: 15
                                                                                                                                            82.6%;
80.0%;
TYPE: PRT
ORGANISM: Artificial Sequence
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1 EAAKYEAYKAAAAA 15
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1 EKAKEEAYKAAAAA 15
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Best Local Similarity 80.0 Matches 12, Conservative
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nes 13; Conservative
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Gaps

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Indels

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US-10-056-583-66

Sequence 66, Application US/10056583

Sequence 66, Application US/10056583

Publication No. US20030064915A1

GENERAL INFORMATION:

APPLICANT: Presidents and Fellows of Harvard College

APPLICANT: Strominger, Jack L.

APPLICANT: Fitches Hareli, Masha

TITLE OF INVENTION: THERAPEUTIC PEPTIDES FOR DEMYELINATING

TITLE OF INVENTION: THERAPEUTIC PEPTIDES FOR DEMYELINATING

FILE REFERENCE: 24655-017

CURRENT PILING DATE: 2002-01-24

CURRENT FILING DATE: 2001-01-24

NUMBER OF SEQ ID NOS: 99

SOFTWARE: FREESEQ for Windows Version 4.0

SEQ ID NO 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    , OTHER INFORMATION: The peptide was designed and synthesized.
US-10-056-583-66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 75.4%; Score 52; DB 14; Length 15; Best Local Similarity 73.3%; Pred. No. 0.038; Matches 11; Conservative 2; Mismatches 2; Indels
             Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2; Mismatches
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ORGANISM: Artificial Sequence
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ORGANISM: Artificial Sequence
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1 EKPKYEAYKAAAPA 15
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Best Local Similarity 73.3
Matches 11; Conservative
          Matches
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Sequence 57, Application US/10056583

Publication No. US20030064915A1

GENERAL INFORMATION:
APPLICANT: Presidents and Fellows of Harvard College
APPLICANT: Strominger, Jack L.
APPLICANT: Friddis-Hareli, Masha
ITILE OF INVENTION: THERAPEUTIC PEPTIDES FOR DEMYELINATING
FILE REPERRNCE: 2655-017

CURRENT APPLICATION NUMBER: US/10/056,583

CURRENT FILING DATE: 2002-01-24

NUMBER OF SEQ ID NOS: 99

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 57

LENGTH: 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Strondinger, Jack L.
APPLICANT: Strondinger, Jack L.
APPLICANT: Fridkis-Hareli, Masha
TITLE OF INVENTION: CONDITIONS
FILE REFREENCE: 24655-017
CURRENT APPLICATION NUMBER: 05/10/056,583
CURRENT PILING DATE: 2002-01-24
PRIOR PILING DATE: 2001-01-24
NUMBER OF SEQ ID NOS: 99
SOUTHARRE: FastSEQ for Windows Version 4.0
SEQ ID NO 85
LENGTH: 15
; OTHER INFORMATION: The peptide was designed and synthesized. US-10-056-583-91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; OTHER INFORMATION: The peptide was designed and synthesized US-10-056-583-57
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US-10-056-583-85
                                                               Score 56; DB 14; Length 15;
Pred. No. 0.0082;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 76.8%; Score 53; DB 14; Length 15; Best Local Similarity 73.3%; Pred. No. 0.026; Matches 11; Conservative 3; Mismatches 1; Indels
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                                                                                                             2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-10-056-583-85; Application US/10056583; Sequence 85, Application No. US20030064915A1; PUBLICATION NO. US20030064915A1; APPLICANT: Presidents and Fellows of Harvard College
                                                                                                           Mismatches
                                                                 81.2%;
80.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: PRT
ORGANISM: Artificial Seguence
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                                                                                                                                                   1 EKAKFEAFKAAAAA 15
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EEAKYAAYKAAAAAA 15
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                                         Query Match
Best Local Similarity 80.07
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Best Local Similarity
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Gaps

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FEATURE:
; OTHER INFORMATION: The peptide was designed and synthesized.
US-10-056-583-51
                                                                                                                                                       Length 15;
                                                                                                                                                                    2; Indels
                                                                                                                                                      Score 51; DB 14;
Pred. No. 0.056;
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1 EAAKYAAYKAAAAA 15
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RESULT 15
US-10-056-583-53
; Sequence 53, Application US/10056583
; Sequence 53, Application US/10056583
; Publication No. US20030064915A1
; GENERAL INFORMATION:
; APPLICANT: Strominger, Jack L.
; APPLICANT: Strominger, Jack L.
; APPLICANT: Fridkis-Hareli, Masha
; TITLE OF INVENTION: THERAPEUTIC PEPTIDES FOR DEMYELINATING;
; TITLE OF INVENTION: CONDITIONS
; FILE OF INVENTION: CONDITIONS
; FILE REPERBNCE: 24655-017
; CURRENT FILING DATE: 2002-01-24
; PRIOR PILING DATE: 2001-01-24
; NUMBER OF SEQ ID NOS: 99
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 53
LENGTH: 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: PRT:
ORGANISM: Artificial Sequence
FRANTSM: PRATURE:
COTHER INFORMATION: The peptide was designed and synthesized.
US-10-056-583-53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 73.9%; Score 51; DB 14; Length 15; Best Local Similarity 73.3%; Pred. No. 0.056; Matches 11; Conservative 2; Mismatches 2; Indels
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Search completed: March 31, 2005, 02:48:49 Job time : 67.5323 secs g

1 EKAKFEAFKAAAAA 15

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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- protein search, using sw model OM protein

March 31, 2005, 02:26:17; Search time 17.9032 Seconds (without alignments) 80.614 Million cell updates/sec Run on:

US-10-056-583A-95

1 EKAKFEAFKAAAAA 15 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283416 segs, 96216763 residues Searched:

283416 Total number of hits satisfying chosen parameters:

seq length: 0 seq length: 200000000 Minimum DB Maximum DB

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database

PIR_79:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

		من			SUMMARIES	
Result No.	Score	Ouery Match	Query Match Length	DB	п	Description
:	47.5	68.8	189	7	877930	exoskeletal protei
7	47.5	68.8	189	~	S77935	
n	42	6.09	179	N	F97683	ď
4	42	6.09	179	~	AF2908	50S ribosomal prot
2	41	59.4	346	7	C82156	О
9	41	59.4	828	7	F96535	hypothetical prote
7	40		478	~	S04675	H+-transporting tw
80	40		869	~	T32594	hypothetical prote
σ	39		73	7	840015	•
10	39	56.5	113	7	T30041	щ
11	39	56.5	144	~	D83152	hypothetical prote
12	39	56.5	198	N	A12622	conserved hypothet
13	39	56.5	217	~	A97405	hypothetical prote
14	39	56.5	250	~	T51971	proteasome endopep
15	39	56.5	389	~	G87332	hypothetical prote
16	39	56.5	421	7	JV0057	tolA protein - Esc
17	39	56.5	2957	~	T33152	hypothetical prote
18	38	55.1	151	Н	GGICEH	globin CTT-VIII -
19	38	55.1	246	N	B72728	probable ribosomal
20	38	55.1	320	7	S76422	hypothetical prote
21	38	55.1	436	~	T31902	hypothetical prote
22	38	55.1	510	~	S35028	protein PS2 precur
23	38	55.1	525	-	QQBE6	BFLF1 protein - hu
24	37	53.6	231	7	T02585	hypothetical prote
	37	53.6	254	~	H86355	
56	37	53.6	270	~	G82108	hypoth
27	37	53.6	359	~	H95865	4
28	37	53.6	476	7	C72016	
29	37	53.6	476	7	B86609	glycogen synthase

phosphoenolpyruvat cell division cont translation initia translation initia translational endop hypothetical prote 165K protein, skel probable rysp protrinosomal protein translation elonga 1-acyldlycerol-3-p hypothetical prote hypothetical protein	0
AC0364 F75154 E64114 D75546 T34516 S43529 H77927 B77927 C70521 T51011 T51011 R5DOP0 C70410 B6255	A44230
00000000000000000000000000000000000000	8
575 829 829 14430 1653 1652 206 206 207 305 320	321
22222222233333333333333333333333333333	52.2
0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	36
0 6 6 6 6 6 6 7 6 7 6 7 6 7 6 7 6 7 6 7	45

ALIGNMENTS

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exoskeletal protein HACP202A - American lobster (fragment)
C;Species: Homarus americanus (American lobster)
C;Species: Homarus americanus (American lobster)
C;Species: Homarus americanus (American lobster)
C;Date: 33-401-1997 #sequence_revision 01-Aug-1997 #text_change 09-Jul-2004
C;Accession: 877930
R;Nousiainen, M.; Rafn, K.; Skou, L.; Roepstorff, P.; Andersen, S.O.
A;Description: Characterization of exoskeletal proteins from the American lobster, Homaz
A;Reference number: 877925
A;Accession: 877930
A;Accession: S77930
A;Accession: preliminary
A;Molecule type: protein
A;Residues: 1-189 exoto:
A;Cross-references: UNIPROT:Q7M496
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                                                                                                                                                                                                                                                                                                                                                                                                                                               1;
                                                                                                                                                                                                                                                                                                                                                                                             Length 189;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                       68.8%; Score 47.5; DB 2; 75.0%; Pred. No. 1.3; 1; Mismatches 1;
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                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity
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Best Local Simil
Matches 12; C
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exoskeletal protein HACP202B - American lobster (fragment)
C;Species: Homarus americanus (American lobster)
C;Species: Homarus americanus (American lobster)
C;Accession: 877935
R;Nousiainen, M.; Rafn, K.; Skou, L.; Roepstorff, P.; Andersen, S.O.
R;Nousiainen, M.; Rafn, K.; Skou, L.; Roepstorff, P.; Andersen, S.O.
A;Description: Characterization of exoskeletal proteins from the American lobster, Homax A;Reference number: 877925
A;Accession: 877935

A,Status: preliminary
A,Molecule type: procein
A,Reaidues: 1-189 <NOU's
A,Cross-references: UNIPROT:Q7M495

Gaps ï Length 189; 1; Indels Query Match 68.8%; Score 47.5; DB 2; Best Local Similarity 75.0%; Pred. No. 1.3; Matches 12; Conservative 2; Mismatches 1;

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12 |||:|:|||||| ||| 11 EKARFFQAFKAAEAAA 26 1 EKAK-FEAFKAAAAA ద Š

RESULT 3 F97683

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A; Reference number: A82035; MUID: 20406833; PMID: 10952301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    59.4%;
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69.2%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity 90.0
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Best Local Similarity
Matches 9; Conserv
                                                                                                                            A; Status: preliminary A; Molecule type: DNA
                                                                                                    A; Accession: C82156
                                                                                                                                                                                                                                                                                                                                                                                                    A; Map position: 1
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A,Gene: VC1791
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Matches
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A;Cross-references: UNIPROT:Q8UBZ5; GB:AE008688; PIDN:AAL43684.1; PID:g17741210; GSPDB:d
A;Experimental source: strain C58 (Dupont)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C.Accession: AF2008
C.Accession: AF2008
R.Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, I. Rarge, G.; Gillet, W.; Grant, C.; Guenthner, D.; Kutyavin, T.; Levy, R.; Li, M.; McClell; Karp, P.; Romero, P.; Zhang, S.
Science 294, 2317-2323, 2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A.Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm,
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Cyspecies: Cys
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C;Species: Agrobacterium tumefaciens
C;Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 09-Jul-2004
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A,Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.
A,Reference number: AB2577; MUID:21608550; PMID:11743193
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A;Map position: circular chromosome
C;Superfamily: Escherichia coli ribosomal protein L19
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A;Map position: circular chromosome
C;Superfamily: Escherichia coli ribosomal protein L19
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Best Local Similarity 66.7
Matches 10; Conservative
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A;Status: preliminary
A;Molecule type: DNA
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GACCESSION: F96535
RiTheologis, A.; Ecker, J.; Rederspiel, N.A.; Kaul, S.; White, O.; Alonso, Chi, C.W.; Chung, M.F.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.; ansen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000
A.; Athors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C., C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali, Rizzo, M.; Rooney, T.; Rooney, T.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, II ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A,Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A;Reference number: A86141; MUID:21016719; PMID:11130712
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A,Molecule type: DNA
A,Residues: 1-828 <STO>
A,Cross-references: UNIPROT:Q9C6C7; GB:AE005173; NID:g10092168; PIDN:AAG12588,1; GSPDB:GN
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                                                                 NID: 99656310; PIDN: AAF9494(
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C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Mar_2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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A,Residues: 1-346 (HEI>
A,Cross-references: UNIPROT:Q9KR55; GB:AE004256; GB:AE003852; NID:g
A,Experimental source: serogroup O1; strain N16961; biotype El Tor
                                                                                                                                                                                                                                                                                                                          Score 41; DB 2; Length 346;
Pred. No. 25;
1; Mismatches 0; Indels
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Pred. No. 56;
2; Mismatches
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A;Cross-references: UNIPROT:Q19615; EMBL:U53150; PIDN:AAA96131.1; GSPDB:GN00023; CESP:F2
A;Experimental source: strain Bristol N2; clone F20A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Cipecies: Pseudomonas aeruginosa
Cibecies: Pseudomonas aeruginosa
Cibate: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 09-Jul-2004
Cibate: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 09-Jul-2004
Cibate: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 09-Jul-2004
Ristover, C.K.; Phama, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrener, P.; Hickey, M.J.; Br adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Liarbig, K.; Liam, J.; Lory, S.; Olson, M.V.
Nature 406, 959-964, 2000
A;Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic pathc A;Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic pathc A;Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic pathc A;Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic pathc A;Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic pathc A;Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic pathc A;Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic pathc A;Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic pathc A;Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic pathc A;Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic pathc A;Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic pathc A;Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic pathc A;Title: Complete genome sequence of Pseudomonas aeruginosa aeruginosa PA01, an opportunistic pathc A;Title: Complete genome sequence of Pseudomonas aeruginosa aeruginosa pathc A;Title: Complete genome sequence of Pseudomonas aeruginosa aeruginosa pathc A;Title: Complete genome sequence of Pseudomonas aeruginosa aerug
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C;Species: Agrobacterium tumefaciens
C;Date: 11.-Jan.-2002 #sequence_revision 11.-Jan.-2002 #text_change 09-Jul-2004
C;Accession: A12622
R;Mood, D;W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.B.; Chen, Y.; Woo, L erage, G.; Gillet, W.; Grant, C.; Guenthner, D.; Kutyavin, T.; Levy, R.; Li, M.; McClell
S; Karp, P.; Romero, P.; Zhang, S.
Science 294, 2317-2323, 2001
A;Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm, ster, E.W.
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                                                                                                                          C;Species: Caenorhabditis elegans
C;Jote: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: T30041
R;Gattung, S.; Wu, X.
submitted to the EMBL Data Library, March 1996
A;Reference number: 220726
A;Reference number: 220726
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7
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C;Superfamily: Caenorhabditis elegans hypothetical protein F57E7.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    56.5%; Score 39; DB 2; Length 113; llarity 68.8%; Pred. No. 19; Conservative 1; Mismatches 2; Indels
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                                                                                               - Caenorhabditis elegans
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A;Molecule type: DNA
A;Residues: 1-113 <GAT>
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Pred. No. 24;
2; Mismatches
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Best Local Similarity 64.3%;
Matches 9; Conservative
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82 KAQVDAFHAAALAA 95
                                                                                               hypothetical protein F20Al.1
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Best Local Similarity
Matches 11; Conserv
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$40015
phd get P1
C; Species: phage P1
C; Species: phage P1
C; Species: phage P1
C; Date: 25-Dec-1994 #sequence_revision 23-Feb-1996 #text_change 09-Jul-2004
C; Accession: $40015; $38553
R; Lebnherr, H.; Maguin, E.; Jafri, S.; Yarmolinsky, M.B.
J. Mol. Biol. 233, 414-428, 1993
A; Title: Plasmid addiction genes of bacteriophage P1: doc, which causes cell death on cu A; Reference number: $40015; MUID:94016561; PMID:9411153
A; Mocession: $40015
A; Mocession: $40015
A; Residues: 1.73 < LEH>
A; Rocession: Sdols, MUID:94016561; PMID:9463276; PIDN:AA16932.1; PID:9215645
A; Residues: UNIPROT:Q06253; GB:M95666, NID:9463276; PIDN:AA16932.1; PID:9215645
A; Reference number: $38553
A; Molecule type: DNA
A; Reference number: $38553
A; Molecule type: DNA
A; Residues: 1.73 < SGH>
A; Residues: 1.73 < SGH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        hypothetical protein C02B10.5 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: 29-Oct-1999 #text_change 09-Jul-2004
C;Accession: T32594
R;Nelson, J.; White, S.; Hawkins, J.; Wohldmann, P.
submitted to the EMBL. Data Library, December 1997
A;Description: The sequence of C. elegans cosmid C02B10.
A;Reference number: Z21196
A;Reference number: Z21196
A;Reterence number: Z21196
A;Reterence number: Z21196
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Reterences: UNIPROT:O44447; EMBL:AF038605; PIDN:AAB92020.1; GSPDB:GN00022; CESP:A;Experimental source: strain Bristol N2; clone C02B10
C;Genetics:
A;Gene: CESP:CO2B10.5
A;Genetics:
A;Gene: CESP:CO2B10.5
A;Introns: 61/3; 102/2; 188/3; 349/2; 641/1
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F;181-357/Domain: H+-transporting ATP synthase alpha chain homology <ATP>
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                                                                                                                                                                            Indels
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                                                                                      Score 40; DB 2;
Pred. No. 49;
                                                                                                                                                                            2; Mismatches
                                                                                 Query Match 58.0%;
Best Local Similarity 66.7%;
Matches 10; Conservative 2
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464 EEAKAKAAKLAAAA 478
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Matches 9; Conserv
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Search completed: March 31, 2005, 02:42:30 Job time : 18.9032 secs
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                           Best Local Similarity
Matches 10; Conserv
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A;Residues: 1-389 <STO>
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A;Title: The cc...

A;Reference number: AB2577; .....
A;Accession: A12622
A;Accession: A12622
A;Accession: A12622
A;Accession: A12622
A;Accession: Algebraic strain cs (Dupont)
A;Cosereferences: UNIRROT:08UICO; GB:AE008688; PIDN:AAL41399.1; PID:g17738717; GSPDB:CASAperimental source: strain C58 (Dupont)
A;Experimental source: strain C58 (Dupont)
A;Genetico:
A;Genetico:
A;Genetico:
A;Map position: circular chromosome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 13
A97405
hypothetical protein AGR C_660 [imported] - Agrobacterium tumefaciens (strain C58, Cerec Species: Agrobacterium tumefaciens
C;Species: Agrobacterium tumefaciens
C;Date: 30-Sep-2001 #sequence_revision 30-Sep-2001 #text_change 09-Jul-2004
C;Accession: A97405
R;Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Qurollo, B.; Goldman, A.; Liu, F.; Wollam, C.; Allinger, M.; Doughty, D.; Scott, C.; Lappas, C.; Markelz, B.; Science 294, 231-2328, 2001
A;Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium tum A;Reference number: A97359; MUID:21608551; PMID:11743194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-217 <KUR>
A;Cross-references: UNIPROT:Q8UICO; GB:AE007869; PIDN:AAK86194.1; PID:g15155291; GSPDB:G
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R,Fu, H.; Doelling, J.H.; Arendt, C.S.; Hochstrasser, M.; Vierstra, R.D. Genetics 149, 677-692, 1998

A;Title: Molecular organization of the 20S proteasome gene family from A, Reference number: Z25275; MUID:9611183; PMID:9611183
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A;Molecule type: mRNA
A;Residues: 1-250 <FCH3-
A;Cross-treferences: UNIPROT:024616; EMBL:AF043523; PIDN:AAC32059.1
A;Experimental source: strain Columbia; seedling hypocotyls
C;Genetics:
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Pred. No. 35;
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A,Map position: circular chromosome
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Beet Local Similarity 80...
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95 KAKMEAFRAA 104
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114 KAKMEAFRAA 123
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Rivierman, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, J.E. B.; Laub, M.T.; DeBoy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Kolone n. J.; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M. Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001
A; Title: Complete Genome Sequence of Caulobacter crescentus.
A; Reference number: A87249; MUID:21173698; PMID:11259647
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Cross-references: UNIPROT: Q9AAC8; GB: AE005673; NID: g13421893; PIDN: AAK22659.1; GSPDB:GN
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                                                                                                                                                                                                                    hypothetical protein CC0674 [imported] - Caulobacter crescentus
C;Species: Caulobacter crescentus
C;Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 09-Jul-2004
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  Pred. No. 40;
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ilarity 76.9%;
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64.3%;
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Best Local Similarity 64.3
Matches 9; Conservative
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                                                                                                    March 31, 2005, 02:18:02 ; Search time 80.5645 Seconds (without alignments) 95.342 Million cell updates/sec
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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Gapop 10.0 , Gapext 0.5
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PIR; S77935; S77935.

NON TER 18 189

SEQUENCE 189 AA; 20180 MW; 72A4EFCD9C7ECFE9 CRC64;
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Submitted (JUN-1997) to the PIR data bank.
PIR; S77930; S77930;
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Nephropoidea; Nephropidae; Homarus.
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01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
1-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Exoskeletal protein HACP202B (Fragment).
Homarus americanus (American lobster).
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01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Exoskeletal protein HACP202A (Fragment).
Homarus americanus (American lobster).
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                                          Q7XVT5
Q0XXVT5
Q0UICO
Q0W1C0
Q0W1K6
Q7DIK6
Q7DIK6
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Q7DIK6
Q7DIK6
Q7DIK6
Q9CFPSI
Q9VFL4
Q9XZR1
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Q7Y3M5
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11 EKARFFQAFKAAEAAA 26
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189 AA;
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Q7M495;
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Q7M496;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Oryza sativa (japonica cultivar-group).
Wkaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae,
Ehrhartoideae, Oryzeae, Oryza.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 63.8%; Score 44; DB 2; Length 707; 73.3%; Pred. No. 79; 3; Indels
                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 99;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SECUENCE FROM N.A.
Putnam N., Detter J.C., Richardson P.M., Rokhsar D.;
Submitted (AUG-2004) to the EMBL/GenBank/DDBJ databases.
EMBL; AY714833; AAU82834.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sasaki T., Matsumoto T., Katayose Y.;
Submitted (JUN-2002) to the EMBL/GenBank/DDBJ databases.
BMBL; AP005428; BAD28652.1;
GO; 60000777; Emicrotubule associated complex; IEA.
GO; GO:0003777; E:microtubule motor activity; IEA.
GO; GO:0007017; P:microtubule-based process; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hypothetical protein.
SEQUENCE 707 AA; 78670 MW; 104FE803EA51973D CRC64;
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Last annotation update)
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                        ed. No. 6.2;
Mismatches
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                                                                                                                                                                                                                                                                           PRT;
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Pfam; PF01221; Dynein_light; 1.
                          Pred.
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75.0%; EL.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  uncultured archaeon GZfos1D1.
Archaea; environmental samples.
                                                                                                   12
                                                                                                                                                11 EKARFFOAFKAAEAAA 26
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Science 305:1457-1462(2004)
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                                                                                                1 EKAK-FEAFKAAAAAA
                  Best Local Similarity 75.0
Matches 12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity 73.3
les 11; Conservative
                                                                                                                                                                                                                                                                              PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                               ORFNames=GZID1 21.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=286721;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=39947;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PubMed=15353801;
                                                                                                                                                                                                                                                                                                                            25-OCT-2004
25-OCT-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             genomics.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
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                                                                                                                                                                                                                                                                                                      064CP3;
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                                                                                                                                                                                                                                                                           Q64CP3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   QEERTS
                                                                                                                                                                                                                   RESULT 3
064CP3
10 064CP3
10 064CP3
10 064CP3
10 12 5-C
10 12 5-C
10 12 5-C
10 12 5-C
10 12 25-C
10
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REGURACE KNOWN N. SEQUENCE SEN, TOTAL R.A., EVANDE C.A., GGCGATO-G.10. S. Adams C.A., GGCATO-G. D.D., CALLINEER SEN, PARKER S.A., HONKINS R.A., GALLE R.F., Adams C.A., GGCATO-G.C., SCHORTE S.E., HOLL R.A., EVANDE C.A., GGLORGE S.R., SANCHARD G., CADAMS C.C., BACKER S.E., ABRUDATTER M., HENDERSON S.N., BUTCHOR G.G., WORTHAND S.E., RIGHERGE S.G., CHARDER N., PERIFERE B.D., MAN C., ROGERS Y.H.C., BACKER E.G., CHARDE M., PERIFERE B.D., RA BATAGON R.C., ROGERS Y.H.C., BACKER S.G., CHARDE M., PERIFERE B.D., RAN BANIL J.F., AGDAVANIA A., AN H.J., ANDICARCE S. MAINDE G. BALLOW R.M., CANDER S. DANKER S.D., BORTON C., BALLOW R., BORNON D., BOCKAND M. CANDER S., DENCKRED D., BOCKAND M.R., BORNON S., DENCKRED D., BOCKAND M.R., BORNON S., DENCKRED M., CANDER S., DELGER A., CARDITA I., RA BALLOS S., DELGER A., CANDER S., DELGER A., CANDER S., DELGER A., CANDER S., DELGER A., CANDER S., DELGER A., DENG Z., GENER S., CHARDER S., DELGER S.W., BANDER S., GORFEL J.H., GAGIN S., DELGER S., GORFEL S., GENERAL S., CANDER S., DELGER S., GORFEL S., GENERAL S., RANDER S., DELGER S., GORFEL S., GORFEL S., GENERAL S., RANDER S., DELGER S., GORFEL S., GENERAL S., RANDER S., LOIN S., HEIMMEN T.J., HEATHON S., LOIN S., LEVINGER S., KIND D., LAIL S., MARTEL S., KANDER S., LOIN S., MONDER S., KIND D., LAIL S., MARTEL S., KANDER S., KIND D., LAIL S., MARTEL S., MONDER S., KIND D., LAIL S., MARTEL S., MONDER S., KIND D., LAIL S., MARTEL S., MONDER S.,
                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE-22426069; PubMed=12537572;
Misra S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,
Hradecky P., Huang Y., Kaminker J.S., Millburn G.H., Prochnik S.E.,
                           .;
0
                                                                                                                                                                                                                                                                                                                                                                   Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Glover C.V.C., Bidwai A.P., Zhao W.F.;
Submitted (OCT-1996) to the EMBL/GenBank/DDBJ databases.
                           4
                                                                                                                                                                                                                   RL22_DROME STANDARD; PRT; 299 AA. P50887; Q9V3X9; P-10-CT-1996 (Rel. 34, Created) 01-NOV-1997 (Rel. 35, Last sequence update) 25-JAM-2005 (Rel. 46, Last annotation update) Name=RpL22; ORFNames=CG7434;
66.7%; Pred. No. 19; tive 1; Mismatches
                                                                 1 EKAKFEAFKAAAAA 15
                                                                                                        81 ERLSFLLFKAAAAA 95
                    10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENOME REANNOTATION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
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Endopterygota; Diptera; Brachycera; Muscomorpha; a; Drosophilidae; Drosophila.

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SEQUENCE FROM N.A.
MEDLINE=99132306; PubMed=9931508; DOI=10.1016/S0378-1119(98)00529-0;
KOyama Y., Katagiri S., Hanai S., Uchida K., Miwa M.;
"Poly(ADP-ribose) polymerase interacts with novel Drosophila ribosomal proteins, L22 and l23a, with unique histone-like amino-terminal
               Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
                                                                                                                                                                                                                                                                                                                                                            EMBL, AF080131, AAD19341.1; -.
Flybase, FBGR0015288, RpL22.
GO; GO:0005622; C:intracellular; IEA.
GO; GO:0005840; C:ribosome; IEA.
GO; GO:0003735; F:structural constituent of ribosome; IEA.
GO; GO:0003735; F:structural constituent of ribosome; IEA.
Interpro; IPR002671; Ribosomal L22e.
Pfam; PF01776; Ribosomal L22e.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE 312 AA; 32273 MW; 0BE9A15CB473083B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 EKAKFEAFKAAAAA 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       49 ЕКРКАЕААКРАААА 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      11; Conservative
                                                                                                                                                                                                                                                                                                                                       Gene 226:339-345(1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ribosomal protein.
                                                                                                 NCBI_TaxID=7227;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                            STATIN=Oregon.R;
MEDLINE=20196011; PubMed=10731137; DOI=10.1126/science.287.5461.2220;
Benos P.V., Gatt M.K., Ashburner M., Murphy L., Harris D.,
Barrell B.G., Ferraz C., Vidal S., Brun C., Demailles J., Cadieu E.,
Dreano S., Gloux S., Lelaure V., Mottier S., Galibert F., Borkova D.,
Minana B., Kafatos F.C., Louis C., Siden-Kiamos I., Bolshakov S.,
Papagiannakis G., Spanos L., Cox S., Madueno E., de Pablos B.,
Modolell J., Peter A., Schoettler P., Werner M., Mourkioti F.,
Beinert N., Dowe G., Schaefer U., Jaeckle H., Bucheton A.,
Callister D.M., Campbell L.A., Darlamitsou A., Henderson N.S.,
Modillan P.J., Salles C., Tait E.A., Valenti P., Saunders R.D.C.,
Smith C.D., Tupy J.L., Whitfield E.J., Bayraktaroglu L., Berman B.P., Bettencourt B.R., Celniker S.E., de Grey A.D.N.J., Drysdale R.A., Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q., Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                               Annotation of the Drosophila melanogaster euchromatic genome:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "From sequence to chromosome: the tip of the X chromosome of D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -!- SIMILARITY: Belongs to the ribosomal protein L22e family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Poly-Ala.
Poly-Ala.
Poly-Ala.
Poly-Ala.
Poly-Ala.
Poly-Ala.
Poly-Lya.
App/Glu-rich (highly acidic).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4; Indels
                                                                                                                                                                                                            Genome Biol. 3:RESEARCH0083.1-RESEARCH0083.22(2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           62.3%; Scor. 73.3%; Pred. No. 52, 73.3%; O; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FlyBase; FBGN0015288; RpL22.
InterPro; IPR002671; Ribosomal L22e.
Pfan: PF01776; Ribosomal L22e; I.
ProDom; PD007306; Ribosomal_L22e; I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; AE003418; AAF45546.1; -. EMBL; AL132792; CAB60023.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         30610 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; U42587; AAB17433.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Science 287:2220-2222(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 EKAKFEAFKAAAAA 15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      299 AA;
                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ribosomal protein.
                                                                                                                                                                                       ic review
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IntAct; P50887;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             melanogaster.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE
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      RAPARA RA
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Gaps

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2; Length 312; 4; Indels

62.3%; Score 43; DB 73.3%; Pred. No. 55; ative 0; Mismatches

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                                                                                                                                                                                                                                                                                                                                       Capela D., Barloy-Hubler F., Gouzy J., Bothe G., Ampe F., Batut J., Boistard P., Backer A., Boutry M., Cadieu E., Dreano S., Gloux S., Godrie T., Goffeau A., Kahn D., Kise E., Lelaure V., Masuy D., Pohl T., Portetale D., Puehler A., Purnelle B., Ramsperger U., Renard C., Thebault P., Vandenbol M., Weidner S., Galibert F.; Ranaryels of the chromosome sequence of the legume symbiont Sinorhizobium melilori strain 1021.", Proc. Natl. Acad. Sci. U.S.A. 98:9877-9882(2001).

-! FUNCTION: This protein is located at the 305-50S ribosomal subunit interface and may play a role in the structure and function of the aminoacyl-tRNA binding site (By similarity).

-! SIMILARITY: Belongs to the ribosomal protein L199 family.
                                                                                                                                                                                                                                                                                                                    MEDLINE=21396507; PubMed=11481430; DOI=10.1073/pnas.161294398;
                                                                                                                                                                               Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales; Rhizobiaceae; Sinorhizobium/Ensifer group; Sinorhizobium.
                                                                                                          508 ribosomal protein L19.
Name=rpl8; OrderedLocusNames=R03246; ORFNames=SMc03863;
                                                                  28-FEB-2003 (Rel. 41, Last sequence update)
25-OCT-2004 (Rel. 45, Last annotation update)
                                                                                                                                                          Rhizobium meliloti (Sinorhizobium meliloti)
                                             41, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; AL591793; CAC47825.1; -.
STANDARD;
                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                            NCBI_TaxID=382;
                                          28-FEB-2003
28-FEB-2003
RL19 RHIME Q92L39;
```

HAMAP; MF 00402; -; 1.

01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
Ribosomal protein L22 (Fragment).
Name-RDL22; Synonyms=rpl22;
Drosophila melanogaster (Fruit fly).

312 AA.

PRELIMINARY;

Q9UAN1; Q9UAN1

090AN1 1D 09 AC 09 DT 01 DT 01 DE Ri GN Na

RESULT 6

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Gaps

; 0

Indels

4,

1; Mismatches

15

60.9%; Score 42; DB 1; Length 179; 66.7%; Pred. No. 48;

us-10-056-583a-95.rup

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PEAM; PF01245; Ribosomal L19; I.
PRINTS; PR00061; RIBOSOMĀLL19.
ITGREAMS; TIGR01024; rplS bact; 1.
PROSITE; PS01015; RIBOSOMāL L19; 1.
Complete proteome; Ribosomal protein.
SEQUENCE 179 AA; 19474 MW; F3256BA44A5AD2D1 CRC64;
                                                   HAMAP; WF 00402; -; 1.
InterPro; IPR01857; Ribosomal L19.
                                                                                                                                                                                                                                                                                                                              137 EKARLEAEKVAAAQA 151
          EMBL; AE008183; AAK88423.1;
                                                                                                                                                                                                                             Query Match 60.9
Best Local Similarity 66.7
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                1 EKAKFEAFKAAAAA
                          PIR; AF2908; AF2908.
PIR; F97683; F97683.
                                                                                                                                                                                                                                                                                                                                                                                                                                  P58168;
                                                                                                                                                                                                                                                                                                                                                                            RESULT 9
RL19_RHILO
                                                                                                                                                                                                                                                                                                                                                                                                                 RL19
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FINCTION: This protein is located at the 30S-50S ribosomal subunit interface and may play a role in the structure and function of the aminoacyl-tRNA binding site (By similarity).

SIMILARITY: Belongs to the ribosomal protein L19P family.
                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The genome of the natural genetic engineer Agrobacterium tumefaciens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=2160851; PubMed=11743194; DOI=10.1126/science.1066803; Goodner B., Hinkle G., Gattung S., Miller N., Blanchard M., Qurollo B., Goldman B.S., Cao Y., Askenazi M., Halling C., Mullin L., Houmiel K., Gordon J., Vaudin M., Iartchouk O., Epp A., Liu F., Wollam C., Allinger M., Doughty D., Scott C., Lappas C., Markelz B., Flanagan C., Slater S., Cielo C., Slater S., Garcone sequence of the plant pathogen and biotechnology agent Agrobacterium tumefaciens C58."; Science 294:2312-2328(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE-2166855, PubMed=11743193; DOI=10.1126/Science.1066804; Wood D.W., Setubal J.C., Kaul R., Monks D.E., Kitajima J.P., Okutav V.K., Zhou Y., Chen L., Wood G.E., Almeida N.F. Jr., Woo L., Chen Y., Paulsen I.T., Eisen J.A., Karp P.D., Bovee D. Sr., Chapman P., Clendenning J., Deatherage G., Gillet W., Grant C., Kutyavin T., Levy R., Li M.-J., McClelland B., Palmideri A., Carang S., Yoo H., Tao Y., Biddle P., Jung M., Krespan W., Perry M., Gordon-Kamm B., Liao L., Kim S., Hendrick C., Zhao Z.-Y., Dolan M., Nester E.W.;
                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                        Name=rplS; OrderedLocusNames=Atu2703, AGR C 4900;
Agrobacterium tumefaciens (strain CS8 / ATCC 33970).
Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
Rhizobiaceae; Rhizobium/Agrobacterium group; Agrobacterium.
                                                                                                                                                     60.9%; Score 42; DB 1; Length 177; 66.7%; Pred. No. 48;
                                                                                                                                                                                          4; Indels
                                                                                                                     177 AA; 19255 MW; 1BD19D6561AB8F22 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                   28-FEB-2003 (Rel. 41, Last sequence update)
25-OCT-2004 (Rel. 45, Last annotation update)
                                                                                                                                                                                                                                                                                                                                          179 AA
                                                                                                                                                                     66.7%; Pred. No. 48; ive 1; Mismatches
InterPro; IPR001857; Ribosomal L19.
Pfan; PF01245; Ribosomal L19; 1.
PRINTS; PR00061; RIBOSOMALL19.
ProDom; P0002979; Ribosomal L19; 1.
TIGRFAMs; TIGR01024; rplS_bact; 1.
PROSITE; PS01015; RIBOSOMAL L19; 1.
Complete protecome; Ribosomal protein.
SEQUENCE 177 AA; 19255 MW; 1B019965
                                                                                                                                                                                                                                                                                                                                                                          (Rel. 41, Created)
                                                                                                                                                                                                                                                        136 EKARIEAEKVAAAQA 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Science 294:2317-2323(2001).
                                                                                                                                                                                                                    1 EKAKFEAFKAAAAA 15
                                                                                                                                                                                                                                                                                                                                                                                                                         508 ribosomal protein L19
                                                                                                                                                                   Local Similarity 66.7
1es 10; Conservative
                                                                                                                                                                                                                                                                                                                                         STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                       RL19 AGRTS
OSUBZ5;
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ID _RL19_A
                                                                                                                                                                                   Matches
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the Buropan Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FUNCTION: This protein is located at the 30S-50S ribosomal subunit interface and may play a role in the structure and function of the aminoacyl-tRNA binding site (By similarity).
SIMILARITY: Belongs to the ribosomal protein L19P family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Kaneko T., Nakamura Y., Sato S., Asamizu E., Kato T., Sasamoto S., Watanabe A., Idesawa K., Ishikawa A., Kawashima K., Kimura T., Kishida Y., Kiyokawa C., Kohara M., Matsumoto M., Matsuno A., Mochizuki Y., Nakayama S., Nakazaki N., Shimpo S., Sugimoto M., Takeuchi C., Yamada M., Tabata S.; Shimpo S., Sugimoto M., Mesorhizobium loti.";

DNA Res. 7:331-338(2000)
                                                                                                                                                                                                                                                                   Rhizobium loti (Mesorhizobium loti).
Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
Phyllobacteriaceae; Mesorhizobium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 1; Length 181; 49;
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PRINTS; PR00061; RIBOSOMĀLL19.
ProDom; PD002979; Ribosomal L19; 1.
TIGRFAMS; TIGR01024; TP1S Ďact; 1.
PROSITE; PS01015; RIBOSOMĀL L19; 1.
Complete proteome; Ribosomāl protein.
SEQUENCE 181 AA; 19927 MW; AEF19D6593A9E835 CRC64;
                                                                 16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
25-OCT-2004 (Rel. 45, Last annotation update)
Socs ribosomal protein Li9.
Name=rplS; OrderedLocusNames=ml14283;
    181 AA
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HAMAP: MF 00402; -; 1.
HAMAP: MF 00402; -; 1.
InterPro; IPR001857; Ribosomal L19.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
STRAIN-MAFF303099;
MEDLINE=21082930; PubMed=11214968;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; AP003003; BAB50976.1; -.
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STANDARD;
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Best Local Similarity
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EMBL; AE009216; AAL43684.1; -.

Matches

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RESULT 10 QGUK87

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Brwinia carotovora (subsp. atroseptica) (Pectobacterium atrosepticum).
Bacteria, Proteobacteria, Gammaproteobacteria, Enterobacteriales,
Enterobacteriaceae, Pectobacterium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                  PubMed=15263089; DOI=10.1073/pnas.0402424101;
PubMed=15263089; DOI=10.1073/pnas.0402424101;
PubMed=15263089; DOI=10.1073/pnas.0402424101;
PubMed=15263089; DOI=10.1073/pnas.0402424101;
Path. S., Sebaihia M., Pritchard L., Holden M.T.G., Hyman L.J.,
Atkin R., Bason N., Brooks K., Chillingworth T., Clark K., Doggett J.,
Fraser A., Hance Z., Hauser H., Jagels K., Moule S., Norbertczak H.,
Ormond D., Price C., Quail M.A., Sanders M., Walker D., Whitehead S.,
Salmond G.P.C., Birch P.R.J., Parkhill J., Toth I.K.;
"Genome sequence of the enterobacterial phytopathogen Erwinia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PubMed=15288952; DOI=10.1016/j.jbiotec.2004.03.020;
Hansmeier N., Bartels F.W., Ros R., Anselmetti D., Tauch A.,
Publer A., Kalinowski J.;
"Classification of hyper-variable Corynebacterium glutamicum surface-layer proteins by sequence analyses and atomic force microscopy.";
J. Biotechnol. 112:177-193(2004).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Corynebacterium glutamicum (Brevibacterium flavum).
Bacteria, Actinobacteria; Actinobacteridae; Actinomycetales;
Corynebacterineae; Corynebacteriaceae; Corynebacterium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 395;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              .. Acad. Sci. U.S.A. 101:11105-11110(2004)
                                                                                                                                                                                                                 25-OCT-2004 (TrEMBLrel. 28, Created)
25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             60.9%; Score 42; DB 2; 73.3%; Pred. No. 99; tive 0; Mismatches
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                                                                                                                                                                                                                                                                                                   Name=tolA; OrderedLocusNames=ECA1372;
                                                                                                                                                                         PRT;
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EMBL, BX950851; CAG74287.1; -.
InterProy. IPR010528; TolA.
Pfam; PF06519; TolA; 1.
Complete proteome.
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Matches 11; Conservative
                          1 EKAKFEAFKAAAAA
                                                                76 DPATFEAFKAATGVA
                                                                                                                                                                         PRELIMINARY;
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SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                      protein.
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Q6D7F3;
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Viruses; dsDNA viruses, no RNA stage; Caudovirales; Myoviridae.
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EMBL, AY116747; AAQ87289.1;
                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.

Summer E.J., Bomer M.L., Bean E.D., Embry A.E., Mebane L.M.,
Tsou L.L.-C., No B.-G., Gonzalez C.F., Young R.F.;
Submitted (AUG-2003) to the EMBL/GenBank/DDBJ databases.
EMBL, AX368235; AAR89355.1; -.
SEQUENCE 274 AA; 28795 MW; 14419D38C3112965 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
Rhizobiaceae; Rhizobium/Agrobacterium group; Rhizobium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 60.9%; Score 42; DB 2; Length 386; Best Local Similarity 60.0%; Pred. No. 97; Matches 9; Conservative 1; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 60.9%; Score 42; DB 2; Length 274; 71.4%; Pred. No. 71;
  4; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Created)
Last sequence update)
Last annotation update)
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Last annotation update)
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                                                                                                                                                                                           274 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         71.4%; Pred. No. 71; ive 2; Mismatches
  Mismatches
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InterPro, IPR001188; Sperm/putr-bndng.
InterPro, IPR006311; Tat.
                                                                                                                                                                                                                                       Created)
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Plasmid megaplasmid 2.
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(TrEMBLrel. 27, I
(TrEMBLrel. 27, I
                                                                                  EKARIEAEKVAAAQA 150
                                          1 EKAKFEAFKAAAAA 15
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116 KAEIEADKAAAAS 129
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hes 10; Conservative
10; Conservative
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05-JUL-2004
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Name=ORF64;
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SEQUENCE
                                                                                    136
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Matches

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Gaps

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Eukaryota, Metazoa, Arthropoda, Hexapoda, Insecta, Pterygota,
Neoptera, Endopterrygota, Diptera, Nematocera, Culicoidea, Anopheles.
NCBI_TaxID=180454,
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STRAIM=EI TOR NIG651 / Serotype Ol;

MEDLINE=20406833; PubMed=10952301; DOI=10.1038/35020000;

MEDLINE=20406833; PubMed=10952301; DOI=10.1038/35020000;

Heidelberg J.F., Eisten J.A., Nelson W.C., Clayton R.A., Gwinn M.L.,

Dodson R.J., Haft D.H., Hickey E.K., Peterson J.D., Umayam L.A.,

Gill S.R., Nelson K.E., Read T.D., Tettelin H., Richardson D.L.,

Ermolaeva M.D., Vamathevan J.J., Bass S., Qin H., Dragoi I.,

Sellers P., McDonald L.A., Utterback T.R., Fleischmann R.D.,

Nierman W.C., White O., Salzberg S.L., Smith H.O., Colwell R.R.,

Mexalanos J.J., Venter J.C., Fraser C.M.;

cholerae.",
                                                                                                                                                                                                                                                                                                                                                                                           Anopheles Genome Sequencing Consortium;
Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.
-!- CAUTION: The sequence shown here is derived from an EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;
Vibrionaceae; Vibrio.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 344;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 41; DB 2; Length 34%;
Pred. No. 1.3e+02;
Pred. No. 1.2e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     344 AA; 39328 MW; C76C9D9A73D8B619 CRC64;
                                                                                                                                                                    U1-WAR-2004 (TrEMBLrel. 26, Created)
01-WAR-2004 (TrEMBLrel. 26, Last sequence update)
01-WAR-2004 (TrEMBLrel. 26, Last sequence update)
EbiP455 (Fragment).
Name=ebiG455; ORFNames=purer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-007-2000 (TrEMBLrel. 15, Created)
01-007-2000 (TrEMBLrel. 15, Last sequence update)
01-UNN-2003 (TrEMBLrel. 24, Last annotation update)
Hypothetical protein VC1791.
OrderedLocusNames=VC1791;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; AAAB01006298; EAA02717.1; -.
GO; GO:0003998; F:acylphosphatase activity; IEA.
InterPro; IPR001792; Acylphosphatase.
InterPro; IPR001793; Rhodanese-like.
Pfam; PF00581; Rhodanese; 1.
PROSITE; PS50206; RHODANESE_3; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              346 AA
                               3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    59.4%;
             60.08;
                                                                               |:| :||:|| | |
104 EQAAYEAFEAARARA 118
                                                           1 EKAKFEAFKAAAAA 15
             Best Local Similarity 60.0
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4 KFEAFKAAAAAA 15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        75 KFEAFKAALFAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                            preliminary data
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Vibrio cholerae.
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ID Q9KR55
AC Q9KR55;
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Gaps
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                                                                                                       Length 346;
                                                                                                    Score 41; DB 2; Length 346
Pred. No. 1.3e+02;
1; Mismatches 0; Indels
Nature 406:477-483 (2000).
EMBL; AE004256; AAF94940.1; -.
PIR, C02156; C82156.
TIGR; VC1791; -.
Complete proteome; Hypothetical protein.
SEQUENCE 346 AA; 37684 MW; 8482E0264D91A6AA CRC64;
                                                                                                      59.4%;
                                                                                                                               9; Conservative
                                                                                                                                                                                       307 EAFKSAAAAA 316
                                                                                                                                                             6 EAFKAAAAA 15
                                                                                                   Query Match
Best Local Similarity
Matches 9; Conserv
    SABBR
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